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<b>PATENT APPLICATION TRANSMITTAL LETTER</b>	Attorney Docket No.: A-676A
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To the Assistant Commissioner for Patents:  
 In re the patent application of: Christopher J. R. Paszty, Jin Cao, and Jianhua Gong  
 For: Beta-Like Glycoprotein Hormone Polypeptide and Heterodimer

Transmitted herewith are:

- ☒ 143 pages of specification, 20 pages of claim(s) and 1 pages of abstract, totaling 164 pages.
- ☒ 6 sheet(s) of drawings.
- ☒ a declaration by the applicants (3 pgs).
- ☒ 3 pages of sequence listing, Attorney Statement (1 pg), and Sequence Listing Diskette.
- ☐ a certified copy of \_\_\_\_\_
- ☒ Other: Assignment including Recordation Cover Sheet (5 pgs)  
 Information Disclosure Statement including 1449 Forms (5 pgs) and 14 references.

☒ **Preliminarily, please amend the specification by inserting before the first line the following:**

-This application claims the benefit of U.S. Provisional Application No. 60,192,654, filed March 28, 2000, and U.S. Provisional Application No. 60/199,211, filed April 24, 2000, which are hereby incorporated by reference.--

**CLAIMS AS FILED**

For	Number Filed	Number Extra	Rate	Fee
Total Claims	217	- 20 =	197	x \$18.00 = \$3,546.00
Independent Claims	17	- 3 =	14	x \$80.00 = 1,120.00
Multiple Dependent Claims	53			+ \$270.00 = 270.00
Basic Fee				\$710.00 = \$710.00
<b>Total Filing Fee</b>				<b>\$5,646.00</b>

- ☒ Please charge Deposit Account No. 01-0519, in the name of Amgen Inc., in the amount of \$5,646.00. An original and one copy are enclosed.
- ☒ Throughout the prosecution of this application, if any extension of time is necessary, please consider this a request therefor.
- ☒ The Commissioner is hereby authorized to charge any additional filing fees which may be required by the accompanying application, any additional fees which may be required during pendency of this application as required by 37 CFR 1.16 or 1.17, or credit any overpayment to Deposit Account No. 01-0519 throughout the prosecution of this application.

Respectfully submitted,

*Richard J. Mazza*

Richard J. Mazza  
 Attorney/Agent for Applicant(s)  
 Registration No.: 27,657  
 Phone: (805) 447-4112  
 Date: November 27, 2000

Please send all future correspondence to:

U.S. Patent Operations/RJM  
 Dept. 4300, M/S 27-4-A  
 AMGEN INC.  
 One Amgen Center Drive  
 Thousand Oaks, California 91320-1799, USA

**EXPRESS MAIL CERTIFICATE**

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I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" notice under 37 C.F.R. 1.10 on the date indicated above and is addressed to Box Patent Application, Assistant Commissioner for Patents, Washington, D.C. 20231

Lynne Buchsbaum  
 Printed Name

*Lynne Buchsbaum*  
 Signature

BETA-LIKE GLYCOPROTEIN HORMONE POLYPEPTIDE  
AND HETERODIMER

5 This application claims the benefit under Title  
35, United States Code, §199(e) of United States  
provisional application Serial No. 60/192,654, filed  
March 28, 2000, and United States provisional  
application Serial No. 60/199,211, filed April 24,  
2000.

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Field of the Invention

The present invention relates to a novel beta-like  
member (referred to herein as "beta-10" or "β10") of  
15 the glycoprotein hormone family and nucleic acid  
molecules encoding same. The invention also relates to  
a novel heterodimeric glycoprotein hormone comprising  
beta-10 as one of the subunits. The invention also  
relates to vectors, host cells, selective binding  
20 agents, such as antibodies, and methods for producing  
beta-10 polypeptides and beta-10 heterodimers. Also  
provided for are methods for the use of beta-10 and  
beta-10 heterodimers and selective beta-10 and beta-10  
heterodimer binding agents, including methods for the  
25 diagnosis and treatment of disorders associated with  
beta-10 and beta-10 heterodimers.

Background of the Invention

30 As generally accepted in the art, there are  
currently five known glycoprotein hormone polypeptides  
produced in humans: alpha-subunit, TSH-(thyroid  
stimulating hormone)-β-subunit, FSH-(follicle

stimulating hormone)- $\beta$ -subunit, LH-(luteinizing hormone)- $\beta$ -subunit, and CG-(chorionic gonadotropin)- $\beta$ -subunit; Thotakura and Blithe, *Glycobiology*, Volume 5, pages 3-10 (1995); Wondisford et al. in Volume 1, Endocrinology (edited by L. DeGroot), pages 208-217, W. B. Saunders Company, Philadelphia, PA (1995); Moyle and Campbell, in Volume 1, Endocrinology (edited by L. DeGroot), pages 230-241, W. B. Saunders Company, Philadelphia, PA (1995). These polypeptides are produced by single genes, with the exception of the CG- $\beta$ -subunit which is encoded by a multigene cluster composed of six homologous sequences linked to the single LH- $\beta$ -subunit gene on chromosome 19; Bo and Boime, *Journal of Biological Chemistry*, vol. 267, pp. 3179-3184 (1992).

Monomeric alpha-subunit (FAS, or free alpha-subunit) has hormonal activity and is secreted by the pituitary gland and the placenta. FAS has been found to play a role in the differentiation of prolactin producing cells in the pituitary and placenta; see Begeot et al., *Science*, vol. 226, pp. 566-568 (1984), Van-Bael and Denef, *Journal of Neuroendocrinology*, vol. 8, pp. 99-102 (1996), and Moy et al., *Endocrinology*, vol. 137, pp. 1332-1339 (1996); and also to stimulate placental prolactin secretion; see Blithe et al., *Endocrinology*, vol. 129, pp. 2257-2259 (1991).

Alpha-subunit also heterodimerizes with each of the four beta-subunits to form four heterodimeric hormones (TSH, FSH, LH and CG). TSH, FSH and LH are produced in the pituitary, stored in secretion granules, and secreted when the appropriate releasing hormone is produced by the hypothalamus. CG is produced in the placenta and appears to be secreted

- constitutively (it is not stored in secretion granules); see Wondisford et al. in Volume 1, *Endocrinology* (ed. L. DeGroot), pp. 208-217, above, and Hall and Crowley, Jr. in Volume 1, *Endocrinology* (ed. L. DeGroot), pp. 242-258, W. B. Saunders Company, Philadelphia, PA (1995).

- TSH influences basal metabolism by regulating the production of thyroid hormones and is used clinically for enhancing the detection and treatment of thyroid carcinoma; see McEvoy, G.(ed.), *AHFS Drug Information*, pp. 2041-2042, American Society of Health-System Pharmacists, Inc., Bethesda, MD (1998). In addition, diagnostic tests for measuring TSH levels in the blood are commonly used for determining the functional status of the thyroid gland when thyroid gland disorder is suspected.

- FSH and LH play important roles in the maintenance of reproductive function in males and females (i.e., gonadal maturation and gonadal steroid production). CG is involved in the maintenance of pregnancy by stimulating the corpus luteum to produce steroid hormones during the first trimester. FSH, LH and CG are used clinically to treat infertility and also as reagents in assisted reproduction procedures such as in vitro fertilization (IVF); see McEvoy, G.(ed.), *AHFS Drug Information*, pp. 2564-2567, American Society of Health-System Pharmacists, Inc., Bethesda, MD (1998). Diagnostic tests for measuring FSH, LH and CG levels are used for the diagnosis of fertility disorders, as well as to test for pregnancy.

- Naturally occurring metabolites of the above mentioned glycoprotein hormone polypeptides have been

described, such as the  $\beta$ -core fragment which is derived from the beta subunit of CG, but no function has yet been assigned to these metabolites; Moyle and Campbell in Volume 1 *Endocrinology* (ed. L. DeGroot) pp. 230-241, above.

In 1994, the five known glycoprotein hormone polypeptides were placed into the cystine-knot growth factor structural superfamily, based on the crystal structure of human CG; Laphorn et al., *Nature*, vol. 369, pp. 455-61 (1994). This superfamily includes the TGF- $\beta$  (transforming growth factor beta), NGF (nerve growth factor) and PDGF (platelet-derived growth factor) gene families. The cystine-knot is formed by three intramolecular disulfide bonds, has a very characteristic structure, and is responsible for the overall three-dimensional structure of all of the members of the superfamily; Isaacs, *Current Opinion in Structural Biology*, vol. 5, pp. 391-395 (1995). A recently published patent application describes a novel member of the cystine-knot family (zsig51); Sheppard and Lok, (1999) WIPO patent application W099/41377. We have determined that zsig51 is in fact a new alpha-like member of the glycoprotein hormone family and will thus refer to this polypeptide as  $\alpha 2$  or alpha-2.

#### Summary of the Invention

The present invention provides, in part, an isolated secretable human polypeptide (SEQ ID NO: 1) which is a novel beta-like member of the glycoprotein hormone family and is herein designated as "beta-10" or " $\beta 10$ ".

The full length amino acid sequence of human  $\beta 10$  in accordance with this invention is shown in Figure 1. The N-terminal signal peptide predicted for the  $\beta 10$  polypeptide is shown underlined. The asparagine (N) at position 87 of SEQ ID NO: 1 is located within a classic NxT glycosylation motif (where x denotes any amino acid except for proline and T denotes threonine) and is likely to be glycosylated. The signal peptide cleavage site in the  $\beta 10$  amino acid sequence is expected to be within the region of eight amino acids shown boxed in Figure 1. Signal peptide cleavage at the site which is most likely to be the authentic *in vivo* cleavage site is reflected in the sequence of the "mature"  $\beta 10$  polypeptide (SEQ ID NO: 3).

The most likely "mature" form (i.e., processed *in situ* to remove the signal peptide) of  $\beta 10$  polypeptide was run against the NonRedundant Protein database using the computer analysis program known as BLAST to examine homologies (specifically, commonly occurring or "conserved" amino acid residues) to known proteins. The top 112 "hits" were found to be various glycoprotein hormone  $\beta$ -subunits from various mammalian, bird and fish species. These homologies clearly indicated that  $\beta 10$  is a new  $\beta$ -like member of the glycoprotein hormone family.

Further, GAP analysis indicated that the homology of  $\beta 10$  to the four known human glycoprotein hormone  $\beta$ -subunits (mentioned above) was 31-37% identity and 42-48% similarity (see Figure 2A-D, referred to hereinbelow). The mature forms of the four known human  $\beta$  glycoprotein hormone polypeptides contain twelve

cysteine residues, which form six intramolecular disulfide bonds. The mature form of the human  $\beta 10$  polypeptide of the present invention contains ten cysteine residues, which are likely to form five intramolecular disulfide bonds. Using the disulfide bond cysteine pairing of CG- $\beta$  as a model, the most likely disulfide bond cysteine pairing for the five putative disulfide bonds in the  $\beta 10$  polypeptide of this invention is as follows: C12-C60, C26-C75, C36-C91, C40-C93 and C96-C103 of SEQ ID NO: 3 (see also Figure 3).

Based on the logical inclusion of the  $\beta 10$  polypeptide of this invention in the glycoprotein hormone family, this polypeptide could be a monomer (analogous to FAS and  $\beta$ -core fragment) and/or could form a heterodimer with one or more glycoprotein hormone family polypeptides (for example heterodimers  $\alpha/\beta 10$ ,  $\beta 10$ /TSH- $\beta$ ,  $\beta 10$ /LH- $\beta$ ). The  $\beta 10$  polypeptide could also form heterodimers with polypeptides which are distinct from the known glycoprotein hormone polypeptides. Within the cystine-knot growth factor superfamily there are many examples of hormones/growth factors which exist as homodimers. Thus, it is also possible that  $\beta 10$  exists as a homodimer (i.e.,  $\beta 10/\beta 10$ ). Based on these various possibilities, the  $\beta 10$  polypeptide may form more than one hormone (i.e., the  $\beta 10$  hormones).

We used a heterodimerization assay, described further below, to determine that  $\beta 10$  forms a heterodimer with human  $\alpha 2$  polypeptide, described in the above mentioned WO99/41377 patent application, and have

thus discovered and defined a novel heterodimeric glycoprotein hormone,  $\alpha 2/\beta 10$ . Similar to the known heterodimeric glycoprotein hormones (TSH, FSH, LH and CG)  $\alpha 2/\beta 10$  is a heterodimer of an alpha-like  
5 glycoprotein hormone polypeptide and a beta-like glycoprotein hormone polypeptide.

This invention also provides for an isolated nucleic acid molecule comprising a nucleotide sequence  
10 selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO: 2;

(b) a nucleotide sequence encoding the polypeptide set forth in SEQ ID NO: 1;

15 (c) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of (a) or (b), wherein the encoded polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer  
20 thereof; and

(d) a nucleotide sequence complementary to any of (a)-(c).

The invention also provides for an isolated  
25 nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide that is at least about 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 percent identical to the polypeptide as set  
30 forth in SEQ ID NO: 1, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;



(b) a nucleotide sequence encoding an allelic variant or splice variant of the nucleotide sequence set forth in SEQ ID NO: 2, wherein the encoded polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(c) a nucleotide sequence of SEQ ID NO: 2, (a), or (b) encoding a polypeptide fragment of at least about 25 amino acid residues, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(d) a nucleotide sequence of SEQ ID NO: 2 or (a)-(c) comprising a fragment of at least about 16 nucleotides;

(e) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a)-(d), wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof; and

(f) a nucleotide sequence complementary to any of (a)-(d).

The invention further provides for an isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 1 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 1 with at least one amino

acid insertion, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(c) a nucleotide sequence encoding a polypeptide  
5 as set forth in SEQ ID NO: 1 with at least one amino acid deletion, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(d) a nucleotide sequence encoding a polypeptide  
10 as set forth in SEQ ID NO: 1 which has a C- and/or N-terminal truncation, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(e) a nucleotide sequence encoding a polypeptide  
15 as set forth in SEQ ID NO: 1 with at least one modification selected from the group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of  
20 the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(f) a nucleotide sequence of (a)-(e) comprising a fragment of at least about 16 nucleotides;

(g) a nucleotide sequence which hybridizes under  
25 moderately or highly stringent conditions to the complement of any of (a)-(f), wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof; and

(h) a nucleotide sequence complementary to any of  
30 (a)-(e).

The invention also provides for an isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

(a) the mature amino acid sequence set forth in SEQ ID NO: 3, and optionally further comprising an amino-terminal methionine;

(b) an amino acid sequence for an ortholog of SEQ ID NO: 3, wherein the encoded polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(c) an amino acid sequence that is at least about 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 percent identical to the amino acid sequence of SEQ ID NO: 3, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(d) a fragment of the amino acid sequence set forth in SEQ ID NO: 3 comprising at least about 25 amino acid residues, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

(e) an amino acid sequence for an allelic variant or splice variant of either the amino acid sequence as set forth in SEQ ID NO: 3, or at least one of (a)-(c) wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof.

The invention further provides for an isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

(a) the amino acid sequence as set forth in SEQ ID

NO: 3 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

- 5 (b) the amino acid sequence as set forth in SEQ ID NO: 3 with at least one amino acid insertion, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

- (c) the amino acid sequence as set forth in SEQ ID  
10 NO: 3 with at least one amino acid deletion, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof;

- (d) the amino acid sequence as set forth in SEQ ID  
NO: 3 which has a C- and/or N-terminal truncation,  
15 wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof; and

- (e) the amino acid sequence as set forth in SEQ ID  
NO: 3, with at least one modification selected from the  
20 group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of the polypeptide of SEQ ID NO: 3 or homodimer or heterodimer thereof.

25

Also provided are fusion polypeptides comprising the amino acid sequences of (a)-(e) above.

- The present invention also provides for an  
30 expression vector comprising the isolated nucleic acid molecules as set forth herein, recombinant host cells comprising recombinant nucleic acid molecules as set

forth herein, and a method of producing a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer of this invention comprising culturing the host cells and optionally isolating the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer so produced.

A transgenic non-human animal comprising a nucleic acid molecule(s) encoding a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer of this invention is also encompassed by the invention. The nucleic acid molecules are introduced into the animal in a manner that allows expression and increased levels of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer, which may include increased circulating levels. The transgenic non-human animal is preferably a mammal.

Also provided are derivatives of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer, or  $\beta 10$  heterodimer of the present invention.

Additionally provided are selective binding agents such as antibodies and peptides capable of specifically binding the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer of the invention. Such antibodies and peptides may be agonistic or antagonistic.

Pharmaceutical compositions comprising the nucleotides,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer, or selective binding agents of the present invention and one or more pharmaceutically acceptable formulation agents are also encompassed by the

invention. The pharmaceutical compositions are used to provide therapeutically effective amounts of the nucleotides or polypeptides of the present invention. The invention is also directed to methods of using the

5 nucleic acid molecules,  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer,  $\beta$ 10 heterodimer and selective binding agents.

The nucleic acid molecules,  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer,  $\beta$ 10 heterodimer and selective binding agents

10 of the present invention may be used to treat, prevent, ameliorate, and/or detect diseases and disorders, including those recited herein.

The present invention also provides a method of

15 assaying test molecules to identify a test molecule which binds to a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. The method comprises contacting the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer with a test molecule and determining the extent of binding of

20 the test molecule to the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. The method further comprises determining whether such test molecules are agonists or antagonists of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. The present invention further

25 provides a method of testing the impact of molecules on the expression of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer or on the activity of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer.

30 Methods of regulating expression and modulating (i.e., increasing or decreasing) levels of a  $\beta$ 10

polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer of this invention are also encompassed by the invention. One method comprises administering to an animal a nucleic acid molecule(s) encoding such a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. In another method, a nucleic acid molecule comprising elements that regulate or modulate expression of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer of this invention may be administered. Examples of these methods include gene therapy, cell therapy, and anti-sense therapy as further described herein.

#### Brief Description of the Figures

FIGURE 1 depicts in linear array the full coding region of human  $\beta$ 10 polypeptide in accordance with this invention (SEQ ID NO: 1). The predicted signal peptide region is underlined and the region containing the predicted signal peptide cleavage site is boxed. The asparagine (N) residue that is located within the classic N<sub>x</sub>T glycosylation motif, and which is very likely to be glycosylated, is shown in larger font. The corresponding nucleic acid sequence which encodes this polypeptide (SEQ ID NO: 2) comprises nucleotides 1-390, inclusive, of the nucleic acid sequence shown in this Figure.

FIGURE 2A-2D illustrates the relatedness of the known human glycoprotein hormone  $\beta$ -subunit polypeptides (prior art) and the  $\beta$ 10 polypeptide of this invention. The mature form of  $\beta$ 10 used for these comparisons (SEQ ID NO: 3) most likely represents the authentic *in vivo* form of  $\beta$ 10 polypeptide. Figures 2A-D comprise the GAP

output showing the amino acid homology between the mature form of  $\beta 10$  and respectively, TSH-(thyroid stimulating hormone)- $\beta$ -subunit, FSH-(follicle stimulating hormone)- $\beta$ -subunit, LH-(luteinizing hormone)- $\beta$ -subunit, and CG-(chorionic gonadotropin)- $\beta$ -subunit.

FIGURE 3 shows the likely disulfide bond cysteine (C) pairs of the five putative disulfide bonds in the most likely mature form of human  $\beta 10$  (SEQ ID NO: 3). The ten cysteine residues are shown in large font and the disulfide bonds are drawn as solid lines. The three disulfide bonds (C12-C60, C36-C91, C40-C93) that form the cystine-knot are drawn above the amino acid sequence, and the two additional disulfide bonds (C26-C75, C96-C103) are drawn below the amino acid sequence.

#### Detailed Description of the Invention

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All references cited in this application are expressly incorporated by reference herein.

#### Definitions

The terms " $\beta 10$  gene" or " $\beta 10$  nucleic acid molecule" or "polynucleotide" refers to a nucleic acid molecule comprising or consisting of a nucleotide sequence as set forth in SEQ ID NO: 2, a nucleotide sequence encoding the polypeptide as set forth in SEQ



ID NO: 1, a nucleotide of the DNA insert in ATCC deposit no. PTA-1210, and nucleic acid molecules as defined herein.

5       The term " $\beta$ 10 polypeptide" refers to a polypeptide comprising the amino acid sequence of SEQ ID NO: 3, and related polypeptides. Related polypeptides include:  $\beta$ 10 polypeptide allelic variants,  $\beta$ 10 polypeptide orthologs,  $\beta$ 10 polypeptide splice variants,  $\beta$ 10  
10 polypeptide variants and  $\beta$ 10 polypeptide derivatives.  $\beta$ 10 polypeptides may be mature polypeptides, as defined herein, and may or may not have an amino terminal methionine residue, depending on the method by which they are prepared.

15       The term " $\beta$ 10 polypeptide allelic variant" refers to one of several possible naturally occurring alternate forms of a gene occupying a given locus on a chromosome of an organism or a population of organisms.

20       The term " $\beta$ 10 polypeptide derivatives" refers to the polypeptide set forth in SEQ ID NO: 3, polypeptide allelic variants thereof, polypeptide orthologs thereof, polypeptide splice variants thereof, or  
25 polypeptide variants thereof, as defined herein, that have been chemically modified.

30       The term " $\beta$ 10 polypeptide fragment" refers to a polypeptide that comprises a truncation at the amino terminus (with or without a leader sequence) and/or a truncation at the carboxy terminus of the polypeptide set forth in SEQ ID NO: 3, polypeptide allelic variants

thereof, polypeptide orthologs thereof, polypeptide splice variants thereof and/or a polypeptide variant thereof having one or more amino acid additions or substitutions or internal deletions (wherein the resulting polypeptide is at least 6 amino acids or more in length) as compared to the  $\beta$ 10 polypeptide amino acid sequence set forth in SEQ ID NO: 3. Polypeptide fragments may result from alternative RNA splicing or from *in vivo* protease activity. In preferred embodiments, truncations comprise about 10 amino acids, or about 20 amino acids, or about 50 amino acids, or about 75 amino acids, or about 100 amino acids, or more than about 100 amino acids. The polypeptide fragments so produced will comprise about 25 contiguous amino acids, or about 50 amino acids, or about 75 amino acids, or about 100 amino acids, or about 150 amino acids, or about 200 amino acids. Such polypeptide fragments may optionally comprise an amino terminal methionine residue. It will be appreciated that such fragments can be used, for example, to generate antibodies to  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer.

The term " $\beta$ 10 fusion polypeptide" refers to a fusion of one or more amino acids (such as a heterologous peptide or polypeptide) at the amino or carboxy terminus of the polypeptide set forth in SEQ ID NO: 3, polypeptide allelic variants, polypeptide orthologs, polypeptide splice variants, or polypeptide variants having one or more amino acid deletions,

substitutions or internal additions as compared to the  $\beta$ 10 polypeptide amino acid sequence set forth in SEQ ID NO: 3.

5       The term " $\beta$ 10 polypeptide ortholog" refers to a polypeptide from another species that corresponds to the  $\beta$ 10 polypeptide amino acid sequence set forth in SEQ ID NO: 3. For example, mouse and human  $\beta$ 10 polypeptides are considered orthologs of each other.

10

      The term " $\beta$ 10 polypeptide splice variant" refers to a nucleic acid molecule, usually RNA, which is generated by alternative processing of intron sequences in an RNA transcript of the  $\beta$ 10 polypeptide amino acid  
15       sequence set forth in SEQ ID NO: 3.

      The term " $\beta$ 10 polypeptide variants" refers to  $\beta$ 10-like polypeptides comprising amino acid sequences having one or more amino acid sequence substitutions, deletions (such as internal deletions and/or polypeptide fragments), and/or additions (such as internal additions and/or fusion polypeptides) as compared to the  $\beta$ 10 polypeptide amino acid sequence set forth in SEQ ID NO: 3. Variants may be naturally  
20       occurring (e.g.,  $\beta$ 10-like polypeptide allelic variants, polypeptide orthologs and polypeptide splice variants) or artificially constructed. Such polypeptide variants may be prepared from the corresponding nucleic acid molecules having a DNA sequence that varies accordingly  
25       from the DNA sequence set forth in SEQ ID NO: 2. In preferred embodiments, the variants have from 1 to 3, or from 1 to 5, or from 1 to 10, or from 1 to 15, or  
30

from 1 to 20, or from 1 to 25, or from 1 to 50, or from 1 to 75, or from 1 to 100, or more than 100 amino acid substitutions, insertions, additions and/or deletions, wherein the substitutions may be conservative, or non-conservative, or any combination thereof.

The term " $\beta$ 10 homodimer" refers to a homodimer of  $\beta$ 10 polypeptides.

10 The term " $\beta$ 10 heterodimer" refers to a heterodimer of the  $\beta$ 10 polypeptide and another polypeptide. An example is the  $\alpha$ 2/ $\beta$ 10 heterodimer which is described further below.

15 The term "antigen" refers to a molecule or a portion of a molecule capable of being bound by a selective binding agent, such as an antibody, and additionally capable of being used in an animal to produce antibodies capable of binding to an epitope of  
20 that antigen. An antigen may have one or more epitopes.

The term "biologically active  $\beta$ 10 polypeptides" refers to  $\beta$ 10-like polypeptides having at least one  
25 activity characteristic of the polypeptide comprising the amino acid sequence of SEQ ID NO: 3 or homo- or heterodimer thereof.

The terms "effective amount" and "therapeutically  
30 effective amount" each refer to the amount of a  $\beta$ 10 nucleic acid molecule or a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer of this invention used to

support an observable level of one or more biological activities of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer described herein.

5       The term "expression vector" refers to a vector which is suitable for use in a host cell and contains nucleic acid sequences which direct and/or control the expression of heterologous nucleic acid sequences. Expression includes, but is not limited to, processes  
10   such as transcription, translation, and RNA splicing, if introns are present.

      The term "host cell" is used to refer to a cell which has been transformed, or is capable of being  
15   transformed with a nucleic acid sequence and then of expressing a selected gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent, so long as the selected  
20   gene is present.

      The term "identity" as known in the art, refers to a relationship between the sequences of two or more polypeptide molecules or two or more nucleic acid  
25   molecules, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between nucleic acid molecules or polypeptides, as the case may be, as determined by the match between strings of two or more nucleotide or two  
30   or more amino acid sequences. "Identity" measures the percent of identical matches between the smaller of two

or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (i.e., "algorithms").

5           The term "similarity" is a related concept, but in contrast to "identity", refers to a measure of similarity which includes both identical matches and conservative substitution matches. If two polypeptide sequences have, for example, 10/20 identical amino acids, and the remainder are all non-conservative substitutions, then the percent identity and similarity would both be 50%. If in the same example, there are 5 more positions where there are conservative substitutions, then the percent identity remains 50%,  
10 but the per cent similarity would be 75% (15/20). Therefore, in cases where there are conservative substitutions, the degree of similarity between two polypeptides will be higher than the percent identity between those two polypeptides.

20

          The term "isolated nucleic acid molecule" refers to a nucleic acid molecule of the invention that is free from at least one contaminating nucleic acid molecule with which it is naturally associated.  
25 Preferably, the isolated nucleic acid molecule of the present invention is substantially free from any other contaminating nucleic acid molecule(s) or other contaminants that are found in its natural environment which would interfere with its use in polypeptide  
30 production or its therapeutic, diagnostic, prophylactic or research use.

The term "isolated polypeptide" refers to a polypeptide of the present invention that is free from at least one contaminating polypeptide or other contaminants that are found in its natural environment. Preferably, the isolated polypeptide is substantially free from any other contaminating polypeptides or other contaminants that are found in its natural environment which would interfere with its therapeutic, diagnostic, prophylactic or research use.

The term "mature  $\beta$ 10 polypeptide" refers to a  $\beta$ 10 polypeptide lacking a leader sequence. A mature  $\beta$ 10 polypeptide may also include other modifications such as proteolytic processing of the amino terminus (with or without a leader sequence) and/or the carboxy terminus, cleavage of a smaller polypeptide from a larger precursor, N-linked and/or O-linked glycosylation, and the like.

The term "nucleic acid sequence" or "nucleic acid molecule" refers to a DNA or RNA sequence. The term encompasses molecules formed from any of the known base analogs of DNA and RNA such as, but not limited to 4-acetylcytosine, 8-hydroxy-N6-methyladenosine, aziridinyl-cytosine, pseudoisocytosine, 5-(carboxyhydroxymethyl) uracil, 5-fluorouracil, 5-bromouracil, 5-carboxymethylaminomethyl-2-thiouracil, 5-carboxy-methylaminomethyluracil, dihydrouracil, inosine, N6-iso-pentenyladenine, 1-methyladenine, 1-methylpseudouracil, 1-methylguanine, 1-methylinosine, 2,2-dimethyl-guanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-methyladenine, 7-methylguanine, 5-methylaminomethyluracil, 5-

methoxyamino-methyl-2-thiouracil, beta-D-mannosylqueosine, 5' -methoxycarbonyl-methyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic  
5 acid, oxybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, N-uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, and 2,6-diaminopurine.

10

The term "naturally occurring" or "native" when used in connection with biological materials such as nucleic acid molecules, polypeptides, host cells, and the like, refers to materials which are found in nature  
15 and are not manipulated by man. Similarly, "non-naturally occurring" or "non-native" as used herein refers to a material that is not found in nature or that has been structurally modified or synthesized by man.

20

The term "operably linked" is used herein to refer to an arrangement of flanking sequences wherein the flanking sequences so described are configured or assembled so as to perform their usual function. Thus,  
25 a flanking sequence operably linked to a coding sequence may be capable of effecting the replication, transcription and/or translation of the coding sequence. For example, a coding sequence is operably linked to a promoter when the promoter is capable of  
30 directing transcription of that coding sequence. A flanking sequence need not be contiguous with the coding sequence, so long as it functions correctly. Thus, for example, intervening untranslated yet



transcribed sequences can be present between a promoter sequence and the coding sequence and the promoter sequence can still be considered "operably linked" to the coding sequence.

5

The term "pharmaceutically acceptable carrier" or "physiologically acceptable carrier" as used herein refers to one or more formulation materials suitable for accomplishing or enhancing the delivery of a  $\beta$ 10 nucleic acid molecule,  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer,  $\beta$ 10 heterodimer or selective binding agents of the present invention as a pharmaceutical composition.

The term "selective binding agent" refers to a molecule or molecules having specificity for the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer and/or  $\beta$ 10 heterodimer of this invention. As used herein, the terms, "specific" and "specificity" refer to the ability of the selective binding agents to bind to human  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer and/or  $\beta$ 10 heterodimer and not to bind to human non- $\beta$ 10 polypeptide, non- $\beta$ 10 homodimer and/or non- $\beta$ 10 heterodimer. It will be appreciated, however, that the selective binding agents may also bind orthologs of the polypeptide set forth in SEQ ID NO: 3, orthologs of human  $\beta$ 10 homodimer and/or orthologs of human  $\beta$ 10 heterodimer, that is, interspecies versions thereof, such as mouse and rat polypeptides.

The term "transduction" is used to refer to the transfer of genes from one bacterium to another,

usually by a phage. "Transduction" also refers to the acquisition and transfer of eukaryotic cellular sequences by retroviruses.

5       The term "transfection" is used to refer to the uptake of foreign or exogenous DNA by a cell, and a cell has been "transfected" when the exogenous DNA has been introduced inside the cell membrane. A number of transfection techniques are well known in the art and  
10   are disclosed herein. See, for example, Graham et al., *Virology*, 52:456 (1973); Sambrook et al., *Molecular Cloning, a laboratory Manual*, Cold Spring Harbor Laboratories (New York, 1989); Davis et al., *Basic Methods in Molecular Biology*, Elsevier, 1986; and Chu  
15   et al., *Gene*, 13:197 (1981). Such techniques can be used to introduce one or more exogenous DNA moieties into suitable host cells.

20       The term "transformation" as used herein refers to a change in a cell's genetic characteristics, and a cell has been transformed when it has been modified to contain a new DNA. For example, a cell is transformed where it is genetically modified from its native state. Following transfection or transduction, the  
25   transforming DNA may recombine with that of the cell by physically integrating into a chromosome of the cell, may be maintained transiently as an episomal element without being replicated, or may replicate independently as a plasmid. A cell is considered to  
30   have been stably transformed when the DNA is replicated with the division of the cell.

The term "vector" is used to refer to any molecule (e.g., nucleic acid, plasmid, or virus) used to transfer coding information to a host cell.

5 Relatedness of Nucleic Acid Molecules  
and/or Polypeptides

It is understood that related nucleic acid molecules include allelic or splice variants of the  
10 nucleic acid molecule of SEQ ID NO: 2, and include sequences which are complementary to any of the above nucleotide sequences. Related nucleic acid molecules also include a nucleotide sequence encoding a polypeptide comprising or consisting essentially of a  
15 substitution, modification, addition and/or a deletion of one or more amino acid residues compared to the polypeptide in SEQ ID NO: 1.

Fragments include nucleic acid molecules which  
20 encode a polypeptide of at least about 25 amino acid residues, or about 50, or about 75, or about 100, or greater than about 100 amino acid residues of the polypeptide of SEQ ID NO: 1.

25 In addition, related  $\beta$ 10 nucleic acid molecules include those molecules which comprise nucleotide sequences which hybridize under moderately or highly stringent conditions as defined herein with the fully complementary sequence of the nucleic acid molecule of  
30 SEQ ID NO: 2, or of a molecule encoding a polypeptide, which polypeptide comprises the amino acid sequence of SEQ ID NO: 1, or of a nucleic acid fragment as defined herein, or of a nucleic acid fragment encoding a

polypeptide as defined herein. Hybridization probes may be prepared using the  $\beta$ 10 sequences provided herein to screen cDNA, genomic or synthetic DNA libraries for related sequences. Regions of the DNA and/or amino acid sequence of the  $\beta$ 10 polypeptide that exhibit significant identity to known sequences are readily determined using sequence alignment algorithms as described herein and those regions may be used to design probes for screening.

10

The term "highly stringent conditions" refers to those conditions that are designed to permit hybridization of DNA strands whose sequences are highly complementary, and to exclude hybridization of significantly mismatched DNAs. Hybridization stringency is principally determined by temperature, ionic strength, and the concentration of denaturing agents such as formamide. Examples of "highly stringent conditions" for hybridization and washing are 0.015M sodium chloride, 0.0015M sodium citrate at 65-68°C or 0.015M sodium chloride, 0.0015M sodium citrate, and 50% formamide at 42°C. See Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup> Ed., Cold Spring Harbor Laboratory, (Cold Spring Harbor, N.Y. 1989); Anderson et al., *Nucleic Acid Hybridisation: a practical approach*, Ch. 4, IRL Press Limited (Oxford, England).

More stringent conditions (such as higher temperature, lower ionic strength, higher formamide, or other denaturing agent) may also be used, however, the rate of hybridization will be affected. Other agents may be included in the hybridization and washing

buffers for the purpose of reducing non-specific and/or background hybridization. Examples are 0.1% bovine serum albumin, 0.1% polyvinyl-pyrrolidone, 0.1% sodium pyrophosphate, 0.1% sodium dodecylsulfate (NaDodSO<sub>4</sub> or SDS), ficoll, Denhardt's solution, sonicated salmon sperm DNA (or other non-complementary DNA), and dextran sulfate, although other suitable agents can also be used. The concentration and types of these additives can be changed without substantially affecting the stringency of the hybridization conditions. Hybridization experiments are usually carried out at pH 6.8-7.4, however, at typical ionic strength conditions, the rate of hybridization is nearly independent of pH. See Anderson et al., Nucleic Acid Hybridisation: a Practical Approach, Ch. 4, IRL Press Limited (Oxford, England).

Factors affecting the stability of a DNA duplex include base composition, length, and degree of base pair mismatch. Hybridization conditions can be adjusted by one skilled in the art in order to accommodate these variables and allow DNAs of different sequence relatedness to form hybrids. The melting temperature of a perfectly matched DNA duplex can be estimated by the following equation:

$$T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{Na}^+]) + 0.41(\% \text{G+C}) - 600/N - 0.72(\% \text{formamide})$$

where N is the length of the duplex formed, [Na<sup>+</sup>] is the molar concentration of the sodium ion in the hybridization or washing solution, %G+C is the percentage of (guanine+cytosine) bases in the hybrid.

For imperfectly matched hybrids, the melting temperature is reduced by approximately 1°C for each 1% mismatch.

5       The term "moderately stringent conditions" refers to conditions under which a DNA duplex with a greater degree of base pair mismatching than could occur under "highly stringent conditions" is able to form. Examples of typical "moderately stringent conditions" are 0.015M sodium chloride, 0.0015M sodium citrate at 10       50-65°C or 0.015M sodium chloride, 0.0015M sodium citrate, and 20% formamide at 37-50°C. By way of example, a "moderately stringent" condition of 50°C in 0.015 M sodium ion will allow about a 21% mismatch.

15       It will be appreciated by those skilled in the art that there is no absolute distinction between "highly" and "moderately" stringent conditions. For example, at 0.015M sodium ion (no formamide), the melting 20       temperature of perfectly matched long DNA is about 71°C. With a wash at 65°C (at the same ionic strength), this would allow for approximately a 6% mismatch. To capture more distantly related sequences, one skilled in the art can simply lower the temperature 25       or raise the ionic strength.

A good estimate of the melting temperature in 1M NaCl\* for oligonucleotide probes up to about 20 nucleotides is given by:

30        $T_m = 2^\circ\text{C per A-T base pair} + 4^\circ\text{C per G-C base pair}$

\*The sodium ion concentration in 6X salt sodium citrate (SSC) is 1M. See Suggs *et al.*, Developmental

Biology Using Purified Genes, p. 683, Brown and Fox (eds.) (1981).

High stringency washing conditions for  
5 oligonucleotides are usually at a temperature of 0-5°C below the T<sub>m</sub> of the oligonucleotide in 6X SSC, 0.1% SDS.

In another embodiment, related nucleic acid  
10 molecules comprise or consist of a nucleotide sequence that is about 70 percent identical to the nucleotide sequence of SEQ ID NO: 2, or comprise or consist essentially of a nucleotide sequence encoding a polypeptide that is about 70 percent identical to the  
15 polypeptide of SEQ ID NO: 1. In preferred embodiments, the nucleotide sequences are about 70 percent, 75 percent, 80 percent, or about 85 percent, or about 90 percent, or about 95, 96, 97, 98, or 99 percent identical to the nucleotide sequence as shown in SEQ ID  
20 NO: 2, or the nucleotide sequences encode a polypeptide that is about 70 percent, 75 percent, 80 percent, or about 85 percent, or about 90 percent, or about 95, 96, 97, 98, or 99 percent identical to the polypeptide sequence as set forth in SEQ ID NO: 1.

25 Differences in the nucleic acid sequence may result in conservative and/or non-conservative modifications of the amino acid sequence relative to the amino acid sequence of SEQ ID NO: 1.

30 Conservative modifications to the amino acid sequence of SEQ ID NO: 1 (and the corresponding modifications to the encoding nucleotides) will produce

$\beta$ 10-like polypeptides in accordance with this invention having functional and chemical characteristics similar to those of the naturally occurring  $\beta$ 10 polypeptide hereof. In contrast, substantial modifications in the

5 functional and/or chemical characteristics of the  $\beta$ 10 polypeptide may be accomplished by selecting substitutions in the amino acid sequence of SEQ ID NO: 1 that differ significantly in their effect on maintaining (a) the structure of the molecular backbone

10 in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

15 For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position.

20 Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for "alanine scanning mutagenesis."

Conservative amino acid substitutions also encompass non-naturally occurring amino acid residues which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological

30 systems. These include peptidomimetics, and other reversed or inverted forms of amino acid moieties.

Naturally occurring residues may be divided into classes based on common side chain properties:



- 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- 2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;
- 3) acidic: Asp, Glu;
- 4) basic: His, Lys, Arg;
- 5) residues that influence chain orientation: Gly, Pro; and
- 6) aromatic: Trp, Tyr, Phe.

For example, non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class. Such substituted residues may be introduced into regions of the human  $\beta 10$  polypeptide that are homologous with non-human  $\beta 10$  polypeptide orthologs, or into the non-homologous regions of the molecule.

In making such changes, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is understood in the art. Kyte *et al.*, *J. Mol. Biol.*, 157:105-131 (1982). It is known that certain amino acids may be substituted for other amino acids

having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within  $\pm 2$  is preferred, those which are within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$  are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functionally equivalent protein or peptide thereby created is intended for use in immunological embodiments, as in the present case. The greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, i.e., with a biological property of the protein.

The following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0  $\pm$  1); glutamate (+3.0  $\pm$  1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5  $\pm$  1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within  $\pm 2$  is preferred, those which are within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$  are even

more particularly preferred. One may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

5

Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can  
10 be used to identify important residues of the  $\beta 10$  polypeptide or to increase or decrease the affinity of the  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers described herein.

15 Exemplary amino acid substitutions are set forth in Table I.

Table I  
Amino Acid Substitutions

Original Residues	Exemplary Substitutions	Preferred Substitutions
Ala	Val, Leu, Ile	Val
Arg	Lys, Gln, Asn	Lys
Asn	Gln	Gln
Asp	Glu	Glu
Cys	Ser, Ala	Ser
Gln	Asn	Asn
Glu	Asp	Asp
Gly	Pro, Ala	Ala
His	Asn, Gln, Lys, Arg	Arg
Ile	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys	Arg, 1,4 Diamino-butyric Acid, Gln, Asn	Arg
Met	Leu, Phe, Ile	Leu
Phe	Leu, Val, Ile, Ala, Tyr	Leu
Pro	Ala	Gly
Ser	Thr, Ala, Cys	Thr
Thr	Ser	Ser
Trp	Tyr, Phe	Tyr
Tyr	Trp, Phe, Thr, Ser	Phe
Val	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

A skilled artisan will be able to determine suitable variants of the polypeptides of SEQ ID NOS: 1 or 3 using well known techniques. For identifying suitable areas of the molecule that may be changed without destroying activity, one skilled in the art may target areas not believed to be important for activity. For example, when similar polypeptides with similar activities from the same species or from other species are known, one skilled in the art may compare the amino acid sequence of a  $\beta$ 10 polypeptide to such similar polypeptides. With such a comparison, one can identify residues and portions of the molecules that are conserved among similar polypeptides. It will be appreciated that changes in areas of a  $\beta$ 10 polypeptide that are not conserved relative to such similar polypeptides would be less likely to adversely affect the biological activity and/or structure of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. One skilled in the art would also know that, even in relatively conserved regions, one may substitute chemically similar amino acids for the naturally occurring residues while retaining activity (conservative amino acid residue substitutions). Therefore, even areas that may be important for biological activity or for structure may be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the polypeptide structure.

30

Additionally, one skilled in the art can review structure-function studies identifying residues in

similar polypeptides that are important for activity or structure. In view of such a comparison, one can predict the importance of amino acid residues in a  $\beta$ 10 polypeptide that correspond to amino acid residues that are important for activity or structure in similar polypeptides. One skilled in the art may opt for chemically similar amino acid substitutions for such predicted important amino acid residues of the  $\beta$ 10 polypeptide.

10

One skilled in the art can also analyze the three-dimensional structure and amino acid sequence in relation to that structure in similar polypeptides. In view of that information, one skilled in the art may predict the alignment of amino acid residues of a  $\beta$ 10 polypeptide with respect to its three dimensional structure. One skilled in the art may choose not to make radical changes to amino acid residues predicted to be on the surface of the protein, since such residues may be involved in important interactions with other molecules. Moreover, one skilled in the art may generate test variants containing a single amino acid substitution at each desired amino acid residue. The variants can then be screened using activity assays know to those skilled in the art. Such variants could be used to gather information about suitable variants. For example, if one discovered that a change to a particular amino acid residue resulted in destroyed, undesirably reduced, or unsuitable activity, variants with such a change would be avoided. In other words, based on information gathered from such routine experiments, one skilled in the art can readily determine the amino acids where further substitutions

15

20

25

30

should be avoided either alone or in combination with other mutations.

A number of scientific publications have been devoted to the prediction of secondary structure. See Moulton J., *Curr. Op. in Biotech.*, 7(4):422-427 (1996), Chou et al., *Biochemistry*, 13(2):222-245 (1974); Chou et al., *Biochemistry*, 113(2):211-222 (1974); Chou et al., *Adv. Enzymol. Relat. Areas Mol. Biol.*, 47:45-148 (1978); Chou et al., *Ann. Rev. Biochem.*, 47:251-276 and Chou et al., *Biophys. J.*, 26:367-384 (1979). Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins which have a sequence identity of greater than 30%, or similarity greater than 40% often have similar structural topologies. The recent growth of the protein structural data base (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. See Holm et al., *Nucl. Acid. Res.*, 27(1):244-247 (1999). It has been suggested (Brenner et al., *Curr. Op. Struct. Biol.*, 7(3):369-376 (1997)) that there are a limited number of folds in a given polypeptide or protein and that once a critical number of structures have been resolved, structural prediction will gain dramatically in accuracy.

30

Additional methods of predicting secondary structure include "threading" (Jones, D., *Curr. Opin. Struct. Biol.*, 7(3):377-87 (1997); Sippl et al.,

Structure, 4(1):15-9 (1996)), "profile analysis" (Bowie et al., *Science*, 253:164-170 (1991); Gribskov et al., *Meth. Enzym.*, 183:146-159 (1990); Gribskov et al., *Proc. Nat. Acad. Sci.*, 84(13):4355-4358 (1987)), and  
5 "evolutionary linkage" (See Home, *supra*, and Brenner, *supra*).

Preferred  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer variants in accordance with this invention  
10 include glycosylation variants wherein the number and/or type of glycosylation sites has been altered compared to the amino acid sequence set forth in SEQ ID NO: 1. In one embodiment,  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer variants according to this  
15 invention comprise a greater or a lesser number of N-linked glycosylation sites than the amino acid sequence set forth in SEQ ID NO: 1. An N-linked glycosylation site is characterized by the sequence: Asn-X-Ser or Asn-X-Thr, wherein the amino acid residue designated as  
20 X may be any amino acid residue except proline. The substitution(s) of amino acid residues to create this sequence provides a potential new site for the addition of an N-linked carbohydrate chain. Alternatively, substitutions which eliminate this sequence will remove  
25 an existing N-linked carbohydrate chain. Also provided is a rearrangement of N-linked carbohydrate chains wherein one or more N-linked glycosylation sites (typically those that are naturally occurring) are eliminated and one or more new N-linked sites are  
30 created. Additional preferred  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer variants include cysteine variants, wherein one or more cysteine residues are deleted from or substituted for another amino acid (e.g., serine) as compared to the amino acid sequence



set forth in SEQ ID NO: 1. Cysteine variants are useful when the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer must be refolded into a biologically active conformation such as after the isolation of insoluble inclusion bodies. Cysteine variants generally have fewer cysteine residues than the native protein, and typically have an even number to minimize interactions resulting from unpaired cysteines.

10 In addition, the polypeptide comprising the amino acid sequence of SEQ ID NO: 3 or a polypeptide variant thereof may be fused to a homologous polypeptide to form a homodimer or to a heterologous polypeptide to form a heterodimer. Heterologous peptides and  
15 polypeptides include, but are not limited to: an epitope to allow for the detection and/or isolation of a  $\beta$ 10 fusion polypeptide; a transmembrane receptor protein or a portion thereof, such as an extracellular domain, or a transmembrane and intracellular domain; a  
20 ligand or a portion thereof which binds to a transmembrane receptor protein; an enzyme or portion thereof which is catalytically active; a polypeptide or peptide which promotes oligomerization, such as a leucine zipper domain; a polypeptide with which  $\beta$ 10  
25 normally dimerizes; a polypeptide or peptide which increases stability, such as an immunoglobulin constant region; and a polypeptide which has a therapeutic activity different from the polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 3 or a  
30 polypeptide variant thereof.

Fusions can be made either at the amino terminus or at the carboxy terminus of the polypeptide

comprising the amino acid sequence set forth in SEQ ID NO: 3 or a polypeptide variant. Fusions may be direct with no linker or adapter molecule or indirect using a linker or adapter molecule. A linker or adapter molecule may be one or more amino acid residues, typically up to about 20 to about 50 amino acid residues. A linker or adapter molecule may also be designed with a cleavage site for a DNA restriction endonuclease or for a protease to allow for the separation of the fused moieties. It will be appreciated that once constructed, the fusion polypeptides can be derivatized according to the methods described herein.

In a further embodiment of the invention, the polypeptide comprising the amino acid sequence of SEQ ID NO: 3 or a polypeptide variant is fused to one or more domains of an Fc region of human IgG. Antibodies comprise two functionally independent parts, a variable domain known as "Fab", which binds antigen, and a constant domain known as "Fc", which is involved in effector functions such as complement activation and attack by phagocytic cells. An Fc has a long serum half-life, whereas an Fab is short-lived. Capon et al., *Nature*, 337:525-31 (1989). When constructed together with a therapeutic protein, an Fc domain can provide longer half-life or incorporate such functions as Fc receptor binding, protein A binding, complement fixation and perhaps even placental transfer. *Id.*

Table II summarizes the use of certain Fc fusions known in the art.

Table II  
Fc Fusion with Therapeutic Proteins

Form of Fc	Fusion partner	Therapeutic implications	Reference
IgG1	N-terminus of CD30-L	Hodgkin's disease; anaplastic lymphoma; T-cell leukemia	U.S. Patent No. 5,480,981
Murine Fcγ2a	IL-10	anti-inflammatory; transplant rejection	Zheng et al. (1995), J. Immunol., <u>154</u> : 5590-5600
IgG1	TNF receptor	septic shock	Fisher et al. (1996), N. Engl. J. Med., <u>334</u> : 1697-1702; Van Zee et al., (1996), J. Immunol., <u>156</u> : 2221-2230
IgG, IgA, IgM, or IgE (excluding the first domain)	TNF receptor	inflammation, autoimmune disorders	U.S. Pat. No. 5,808,029, issued September 15, 1998

IgG1	CD4 receptor	AIDS	Capon et al. (1989), Nature <u>337</u> : 525-531
IgG1, IgG3	N-terminus of IL-2	anti-cancer, antiviral	Harvill et al. (1995), Immunotech., <u>1</u> : 95-105
IgG1	C-terminus of OPG	osteoarthritis; bone density	WO 97/23614, published July 3, 1997
IgG1	N-terminus of leptin	anti-obesity	PCT/US 97/23183, filed December 11, 1997
Human Ig Gy1	CTLA-4	autoimmune disorders	Linsley (1991), J. Exp. Med., <u>174</u> :561-569

In one example, all or a portion of the human IgG hinge, CH2 and CH3 regions may be fused at either the

5 N-terminus or C-terminus of a  $\beta$ 10 polypeptide of this invention using methods known to the skilled artisan. The resulting  $\beta$ 10 fusion polypeptide may be purified by use of a Protein A affinity column. Peptides and

10 proteins fused to an Fc region have been found to exhibit a substantially greater half-life *in vivo* than the unfused counterpart. Also, a fusion to an Fc region allows for dimerization/multimerization of the fusion polypeptide. The Fc region may be a naturally

occurring Fc region, or may be altered to improve certain qualities, such as therapeutic qualities, circulation time, reduce aggregation, etc.

- 5           Identity and similarity of related nucleic acid molecules and polypeptides can be readily calculated by known methods. Such methods include, but are not limited to, those described in Computational Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D.W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part 1, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M. Stockton Press, New York, 1991; and Carillo et al., *SIAM J. Applied Math.*, 48:1073 (1988).
- 10
- 15
- 20           Preferred methods to determine identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are described in publicly available computer programs. Preferred computer
- 25   program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package, including GAP (Devereux et al., *Nucl. Acid. Res.*, 12:387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, and FASTA (Altschul et al., *J. Mol. Biol.*, 215:403-410 (1990)). The BLASTX program is publicly available from the National Center for Biotechnology Information (NCBI) and other sources (*BLAST Manual*,
- 30

Altschul et al. NCB/NLM/NIH Bethesda, MD 20894;  
Altschul et al., *supra*). The well known Smith Waterman  
algorithm may also be used to determine identity.

5        Certain alignment schemes for aligning two amino  
acid sequences may result in the matching of only a  
short region of the two sequences, and this small  
aligned region may have very high sequence identity  
even though there is no significant relationship  
10    between the two full length sequences. Accordingly, in  
a preferred embodiment, the selected alignment method  
(GAP program) will result in an alignment that spans at  
least fifty (50) contiguous amino acids of the target  
polypeptide.

15        For example, using the computer algorithm GAP  
(Genetics Computer Group, University of Wisconsin,  
Madison, WI), two polypeptides for which the percent  
sequence identity is to be determined are aligned for  
20    optimal matching of their respective amino acids (the  
"matched span", as determined by the algorithm). A gap  
opening penalty (which is calculated as 3X the average  
diagonal; the "average diagonal" is the average of the  
diagonal of the comparison matrix being used; the  
25    "diagonal" is the score or number assigned to each  
perfect amino acid match by the particular comparison  
matrix) and a gap extension penalty (which is usually  
1/10 times the gap opening penalty), as well as a  
comparison matrix such as PAM 250 or BLOSUM 62 are used  
30    in conjunction with the algorithm. A standard  
comparison matrix (see Dayhoff et al., Atlas of Protein  
Sequence and Structure, vol. 5, supp.3 (1978) for the  
PAM 250 comparison matrix; Henikoff et al., *Proc. Natl.*

Acad. Sci USA, 89:10915-10919 (1992) for the BLOSUM 62 comparison matrix) is also used by the algorithm.

Preferred parameters for a polypeptide sequence  
5 comparison include the following:

- Algorithm: Needleman *et al.*, *J. Mol. Biol.*,  
48:443-453 (1970);
- Comparison matrix: BLOSUM 62 from Henikoff *et al.*, *Proc. Natl. Acad. Sci. USA*, 89:10915-10919  
10 (1992);
- Gap Penalty: 12
- Gap Length Penalty: 4
- Threshold of Similarity: 0

15 The GAP program is useful with the above parameters. The aforementioned parameters are the default parameters for polypeptide comparisons (along with no penalty for end gaps) using the GAP algorithm.

20 Preferred parameters for nucleic acid molecule sequence comparisons include the following:

- Algorithm: Needleman *et al.*, *J. Mol Biol.*, 48:443-453 (1970);
- Comparison matrix: matches = +10, mismatch = 0
- 25 • Gap Penalty: 50
- Gap Length Penalty: 3

The GAP program is also useful with the above parameters. The aforementioned parameters are the  
30 default parameters for nucleic acid molecule comparisons.

Other exemplary algorithms, gap opening penalties, gap extension penalties, comparison matrices, thresholds of similarity, etc. may be used, including those set forth in the Program Manual, Wisconsin Package, Version 9, September, 1997. The particular choices to be made will be apparent to those of skill in the art and will depend on the specific comparison to be made, such as DNA to DNA, protein to protein, protein to DNA; and additionally, whether the comparison is between given pairs of sequences (in which case GAP or BestFit are generally preferred) or between one sequence and a large database of sequences (in which case FASTA or BLASTA are preferred).

## 15 Synthesis

It will be appreciated by those skilled in the art the nucleic acid and polypeptide molecules described herein may be produced by recombinant and other means.

20

## Nucleic Acid Molecules

The nucleic acid molecules encode a polypeptide comprising the amino acid sequence of a  $\beta$ 10 polypeptide of this invention can readily be obtained in a variety of ways including, without limitation, chemical synthesis, cDNA or genomic library screening, expression library screening and/or PCR amplification of cDNA.

30

Recombinant DNA methods used herein are generally those set forth in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory



Press, Cold Spring Harbor, NY (1989), and/or Ausubel et al., eds., *Current Protocols in Molecular Biology*, Green Publishers Inc. and Wiley and Sons, NY (1994).

The present invention provides for nucleic acid  
5 molecules as described herein and methods for obtaining the molecules.

Where a gene encoding the amino acid sequence of a  $\beta$ 10 polypeptide has been identified from one species,  
10 all or a portion of that gene may be used as a probe to identify orthologs or related genes from the same species. The probes or primers may be used to screen cDNA libraries from various tissue sources believed to express the  $\beta$ 10 polypeptide. In addition, part or all  
15 of a nucleic acid molecule having the sequence set forth in SEQ ID NO: 2 may be used to screen a genomic library to identify and isolate a gene encoding the amino acid sequence of a  $\beta$ 10 polypeptide. Typically, conditions of moderate or high stringency will be  
20 employed for screening to minimize the number of false positives obtained from the screen.

Nucleic acid molecules encoding the amino acid sequence of a  $\beta$ 10 polypeptide may also be identified by  
25 expression cloning which employs the detection of positive clones based upon a property of the expressed protein. Typically, nucleic acid libraries are screened by the binding of an antibody or other binding partner (e.g., receptor or ligand) to cloned proteins  
30 which are expressed and displayed on a host cell surface. The antibody or binding partner is modified

with a detectable label to identify those cells expressing the desired clone.

Recombinant expression techniques conducted in accordance with the descriptions set forth below may be followed to produce these polynucleotides and to express the encoded polypeptides. For example, by inserting a nucleic acid sequence which encodes the amino acid sequence of a  $\beta 10$  polypeptide into an appropriate vector, one skilled in the art can readily produce large quantities of the desired nucleotide sequence. The sequences can then be used to generate detection probes or amplification primers. Alternatively, a polynucleotide encoding the amino acid sequence of a  $\beta 10$  polypeptide can be inserted into an expression vector. By introducing the expression vector into an appropriate host, the encoded  $\beta 10$  polypeptide may be produced in large amounts.

Another method for obtaining a suitable nucleic acid sequence is the polymerase chain reaction (PCR). In this method, cDNA is prepared from poly(A)+RNA or total RNA using the enzyme reverse transcriptase. Two primers, typically complementary to two separate regions of cDNA (oligonucleotides) encoding the amino acid sequence of a  $\beta 10$  polypeptide, are then added to the cDNA along with a polymerase such as *Taq* polymerase, and the polymerase amplifies the cDNA region between the two primers.

Another means of preparing a nucleic acid molecule encoding the amino acid sequence of a  $\beta 10$  polypeptide

is chemical synthesis using methods well known to the skilled artisan such as those described by Engels et al., *Angew. Chem. Intl. Ed.*, 28:716-734 (1989). These methods include, *inter alia*, the phosphotriester, 5 phosphoramidite, and H-phosphonate methods for nucleic acid synthesis. A preferred method for such chemical synthesis is polymer-supported synthesis using standard phosphoramidite chemistry. Typically, the DNA encoding the amino acid sequence of a  $\beta$ 10 polypeptide will be 10 several hundred nucleotides in length. Nucleic acids larger than about 100 nucleotides can be synthesized as several fragments using these methods. The fragments can then be ligated together to form the full length nucleotide sequence of a  $\beta$ 10 polypeptide. Usually, the 15 DNA fragment encoding the amino terminus of the polypeptide will have an ATG, which encodes a methionine residue. This methionine may or may not be present on the mature form of the  $\beta$ 10 polypeptide, depending on whether the polypeptide produced in the 20 host cell is designed to be secreted from that cell. Other methods known to the skilled artisan may be used as well.

In certain embodiments, nucleic acid variants 25 contain codons which have been altered for the optimal expression of  $\beta$ 10 polypeptide in a given host cell. Particular codon alterations will depend upon the  $\beta$ 10 polypeptide(s) and host cell(s) selected for expression. Such "codon optimization" can be carried 30 out by a variety of methods, for example, by selecting codons which are preferred for use in highly expressed genes in a given host cell. Computer algorithms which

incorporate codon frequency tables such as "Ecohigh.cod" for codon preference of highly expressed bacterial genes may be used and are provided by the University of Wisconsin Package Version 9.0, Genetics Computer Group, Madison, WI. Other useful codon frequency tables include "Celegans\_high.cod", "Celegans\_low.cod", "Drosophila\_high.cod", "Human\_high.cod", "Maize\_high.cod", and "Yeast\_high.cod".

### Vectors and Host Cells

When contemplating expression of a  $\beta_{10}$  heterodimer (such as  $\alpha_2/\beta_{10}$ ), it should be understood that the  $\beta_{10}$  polypeptide expression vector as well as an expression vector encoding a polypeptide that heterodimerizes with  $\beta_{10}$  (such as  $\alpha_2$ ) can both be introduced (for example, transformed, co-transformed, transfected, co-transfected, transduced, co-transduced) into a host cell, cell line, tissue, organ, animal or plant. It is also understood that introduction of a  $\beta_{10}$  polypeptide expression vector alone into a host cell, cell line, tissue, organ, animal or plant that already produces a polypeptide that heterodimerizes with  $\beta_{10}$  (such as  $\alpha_2$ ) can result in *de novo* or enhanced production of a  $\beta_{10}$  heterodimer (such as  $\alpha_2/\beta_{10}$ ). A  $\beta_{10}$  heterodimer can also be assembled *in vitro* upon incubation of the component polypeptides (such as  $\beta_{10}$  polypeptide and  $\alpha_2$  polypeptide) under suitable conditions [see Blithe and Iles, Endocrinology, volume 136, pages 903-910 (1995)]. The result may be a mixture of  $\beta_{10}$  polypeptide,  $\beta_{10}$  homodimer and  $\beta_{10}$  heterodimer. Each of these products can be isolated in purified form using conventional

methods such as size exclusion chromatography or immunoaffinity chromatography (for example, using anti- $\beta$ 10 polypeptide antibodies, anti- $\beta$ 10 homodimer antibodies or anti- $\beta$ 10 heterodimer antibodies).

5

A nucleic acid molecule encoding the amino acid sequence of a  $\beta$ 10 polypeptide may be inserted into an appropriate expression vector using standard ligation techniques. The vector is typically selected to be functional in the particular host cell employed (*i.e.*, the vector is compatible with the host cell machinery such that amplification of the gene and/or expression of the gene can occur). A nucleic acid molecule encoding the amino acid sequence of a  $\beta$ 10 polypeptide according to this invention may be amplified/expressed in prokaryotic, yeast, insect (baculovirus systems), and/or eukaryotic host cells. Selection of the host cell will depend in part on whether the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer is to be post-translationally modified (*e.g.*, glycosylated and/or phosphorylated). If so, yeast, insect, or mammalian host cells are preferable. For a review of expression vectors, see *Meth. Enz.*, v.185, D.V. Goeddel, ed. Academic Press Inc., San Diego, CA (1990).

25

Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as "flanking sequences" in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more

30

enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

Optionally, the vector may contain a "tag"-encoding sequence, *i.e.*, an oligonucleotide molecule located at the 5' or 3' end of the  $\beta 10$  polypeptide coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis), or other "tag" such as FLAG, HA (hemagglutinin Influenza virus) or *myc* for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer by various means such as using certain peptidases for cleavage.

Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host

cell species or strain), hybrid (i.e., a combination of flanking sequences from more than one source) or synthetic, or the flanking sequences may be native sequences which normally function to regulate  $\beta 10$  polypeptide expression. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

The flanking sequences useful in the vectors of this invention may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein other than the  $\beta 10$  gene flanking sequences will have been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

Where all or only a portion of the flanking sequence is known, it may be obtained using PCR and/or by screening a genomic library with suitable oligonucleotide and/or flanking sequence fragments from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be

accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen® column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. Amplification of the vector to a certain copy number can, in some cases, be important for the optimal expression of  $\beta$ 10 polypeptide. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (Product No. 303-3s, New England Biolabs, Beverly, MA) is suitable for most Gram-negative bacteria and various origins (e.g., SV40, polyoma, adenovirus, vesicular stomatitis virus (VSV) or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it contains the early promoter).

A transcription termination sequence is typically located 3' of the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells



is a G-C rich fragment followed by a poly T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using methods for nucleic acid synthesis such as those described herein.

A selectable marker gene element encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, tetracycline, or kanamycin for prokaryotic host cells, (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex media. Preferred selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. A neomycin resistance gene may also be used for selection in prokaryotic and eukaryotic host cells.

Other selection genes may be used to amplify the gene which will be expressed. Amplification is the process wherein genes which are in greater demand for the production of a protein critical for growth are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and thymidine kinase. The mammalian cell transformants are placed under selection pressure which only the transformants are uniquely adapted to survive by virtue of the selection gene present in the vector. Selection pressure is imposed by culturing the transformed cells

under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to the amplification of both the selection gene and the DNA that encodes a  $\beta 10$

5 polypeptide of this invention. As a result, increased quantities of the  $\beta 10$  polypeptide are synthesized from the amplified DNA.

A ribosome binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the  $\beta 10$  polypeptide to be expressed. The Shine-Dalgarno sequence is varied but is typically a polypurine (i.e., having a high A-G content). Many Shine-Dalgarno sequences have been identified, each of which can be readily synthesized using methods set forth herein and used in a prokaryotic vector.

20 A leader, or signal, sequence may be used to direct the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer out of the host cell. Typically, a nucleotide sequence encoding the signal sequence is positioned in the coding region of a  $\beta 10$  nucleic acid molecule, or directly at the 5' end of a  $\beta 10$  polypeptide coding region. Many signal sequences have been identified, and any of those that are functional in the selected host cell may be used in conjunction with a  $\beta 10$  nucleic acid molecule. Therefore, a signal sequence may be homologous (naturally occurring) or heterologous to a  $\beta 10$  gene or cDNA. Additionally, a

signal sequence may be chemically synthesized using methods described herein. In most cases, the secretion of a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer from the host cell via the presence of a signal peptide will result in the removal of the signal peptide from the secreted  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer. The signal sequence may be a component of the vector, or it may be a part of a  $\beta 10$  nucleic acid molecule that is inserted into the vector.

Included within the scope of this invention is the use of either a nucleotide sequence encoding a native  $\beta 10$  polypeptide signal sequence joined to a  $\beta 10$  polypeptide coding region or a nucleotide sequence encoding a heterologous signal sequence joined to an  $\beta 10$  polypeptide coding region. The heterologous signal sequence selected should be one that is recognized and processed, *i.e.*, cleaved by a signal peptidase, by the host cell. For prokaryotic host cells that do not recognize and process the native  $\beta 10$  polypeptide signal sequence, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, or heat-stable enterotoxin II leaders. For yeast secretion, the native  $\beta 10$  polypeptide signal sequence may be substituted by the yeast invertase, alpha factor, or acid phosphatase leaders. In mammalian cell expression the native signal sequence is satisfactory, although other mammalian signal sequences may be suitable.

In some cases, such as where glycosylation is

desired in a eukaryotic host cell expression system, one may manipulate the various presequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add presequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein) one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the N-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer if the enzyme cuts at such area within the mature polypeptide.

In many cases, transcription of a nucleic acid molecule is increased by the presence of one or more introns in the vector; this is particularly true where a polypeptide is produced in eukaryotic host cells, especially mammalian host cells. The introns used may be naturally occurring within the  $\beta 10$  gene, especially where the gene used is a full length genomic sequence or a fragment thereof. Where the intron is not naturally occurring within the gene (as for most cDNAs), the intron(s) may be obtained from another source. The position of the intron with respect to flanking sequences and the  $\beta 10$  gene is generally important, as the intron must be transcribed to be effective. Thus, when a  $\beta 10$  cDNA molecule is being transcribed, the preferred position for the intron is

3' to the transcription start site, and 5' to the polyA transcription termination sequence. Preferably, the intron or introns will be located on one side or the other (i.e., 5' or 3') of the cDNA such that it does  
5 not interrupt the coding sequence. Any intron from any source, including any viral, prokaryotic and eukaryotic (plant or animal) organisms, may be used to practice this invention, provided that it is compatible with the host cell(s) into which it is inserted. Also included  
10 herein are synthetic introns. Optionally, more than one intron may be used in the vector.

The expression and cloning vectors of the present invention will each typically contain a promoter that  
15 is recognized by the host organism and operably linked to the molecule encoding a  $\beta$ 10 polypeptide. Promoters are untranscribed sequences located upstream (5') to the start codon of a structural gene (generally within about 100 to 1000 base pairs) that control the  
20 transcription of the structural gene. Promoters are conventionally grouped into one of two classes, inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response  
25 to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, initiate continual gene product production; that is, there is little or no control over gene expression.  
30 A large number of promoters, recognized by a variety of potential host cells, are well known. A suitable promoter is operably linked to the DNA encoding a  $\beta$ 10 polypeptide by removing the promoter from the source

DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector. The native  $\beta$ 10 gene promoter sequence may be used to direct amplification and/or expression of a  $\beta$ 10 nucleic acid molecule. A heterologous promoter is preferred, however, if it permits greater transcription and higher yields of the expressed protein as compared to the native promoter, and if it is compatible with the host cell system that has been selected for use.

Promoters suitable for use with prokaryotic hosts include the beta-lactamase and lactose promoter systems; alkaline phosphatase, a tryptophan (trp) promoter system; and hybrid promoters such as the tac promoter. Other known bacterial promoters are also suitable. Their sequences have been published, thereby enabling one skilled in the art to ligate them to the desired DNA sequence(s), using linkers or adapters as needed to supply any useful restriction sites.

Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus (CMV), a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, *e.g.*, heat-shock promoters and the actin promoter.

Additional promoters which may be of interest in controlling  $\beta$ 10 gene transcription include, but are not limited to: the SV40 early promoter region (Bernoist and Chambon, *Nature*, 290:304-310, 1981); the CMV promoter; the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, *Cell*, 22:787-797, 1980); the herpes thymidine kinase promoter (Wagner *et al.*, *Proc. Natl. Acad. Sci. USA*, 78:144-1445, 1981); the regulatory sequences of the metallothioneine gene (Brinster *et al.*, *Nature*, 296:39-42, 1982); prokaryotic expression vectors such as the beta-lactamase promoter (Villa-Kamaroff, *et al.*, *Proc. Natl. Acad. Sci. USA*, 75:3727-3731, 1978); or the tac promoter (DeBoer, *et al.*, *Proc. Natl. Acad. Sci. USA*, 80:21-25, 1983). Also of interest are the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: the elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, *Cell*, 38:639-646, 1984; Ornitz *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 50:399-409 (1986); MacDonald, *Hepatology*, 7:425-515, 1987); the insulin gene control region which is active in pancreatic beta cells (Hanahan, *Nature*, 315:115-122, 1985); the immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, *Cell*, 38:647-658 (1984); Adames *et al.*, *Nature*, 318:533-538 (1985); Alexander *et al.*, *Mol. Cell. Biol.*, 7:1436-1444, 1987); the mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, *Cell*, 45:485-495, 1986); the albumin gene control region which is active in liver (Pinkert

et al., *Genes and Devel.*, 1:268-276, 1987); the  
alphafetoprotein gene control region which is active in  
liver (Krumlauf et al., *Mol. Cell. Biol.*, 5:1639-1648,  
1985; Hammer et al., *Science*, 235:53-58, 1987); the  
5 alpha 1-antitrypsin gene control region which is active  
in the liver (Kelsey et al., *Genes and Devel.*, 1:161-  
171, 1987); the beta-globin gene control region which  
is active in myeloid cells (Mogram et al., *Nature*,  
315:338-340, 1985; Kollias et al., *Cell*, 46:89-94,  
10 1986); the myelin basic protein gene control region  
which is active in oligodendrocyte cells in the brain  
(Readhead et al., *Cell*, 48:703-712, 1987); the myosin  
light chain-2 gene control region which is active in  
skeletal muscle (Sani, *Nature*, 314:283-286, 1985); and  
15 the gonadotropic releasing hormone gene control region  
which is active in the hypothalamus (Mason et al.,  
*Science*, 234:1372-1378, 1986).

An enhancer sequence may be inserted into the  
20 vector to increase the transcription of a DNA encoding  
a  $\beta$ 10 polypeptide of the present invention by higher  
eukaryotes. Enhancers are cis-acting elements of DNA,  
usually about 10-300 bp in length, that act on the  
promoter to increase transcription. Enhancers are  
25 relatively orientation and position independent. They  
have been found 5' and 3' to the transcription unit.  
Several enhancer sequences available from mammalian  
genes are known (e.g., globin, elastase, albumin,  
alpha-feto-protein and insulin). Typically, however,  
30 an enhancer from a virus will be used. The SV40  
enhancer, the cytomegalovirus early promoter enhancer,  
the polyoma enhancer, and adenovirus enhancers are  
exemplary enhancing elements for the activation of



eukaryotic promoters. While an enhancer may be spliced into the vector at a position 5' or 3' to a  $\beta$ 10 nucleic acid molecule, it is typically located at a site 5' from the promoter.

5

Expression vectors of the invention may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences.

10 Where one or more of the desired flanking sequences are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art.

15

Preferred vectors for practicing this invention are those which are compatible with bacterial, insect, and mammalian host cells. Such vectors include, *inter alia*, pCRII, pCR3, and pcDNA3.1 (Invitrogen Company, Carlsbad, CA), pBSII (Stratagene Company, La Jolla, CA), pET15• (Novagen, Madison, WI), pGEX (Pharmacia Biotech, Piscataway, NJ), pEGFP-N2 (Clontech, Palo Alto, CA), pETL (BlueBacII; Invitrogen), pDSR-alpha (PCT Publication No. WO90/14363) and pFastBacDual  
20 (Gibco/BRL, Grand Island, NY).

25

Additional suitable vectors include, but are not limited to, cosmids, plasmids or modified viruses, but it will be appreciated that the vector system must be  
30 compatible with the selected host cell. Such vectors include, but are not limited to plasmids such as Bluescript<sup>®</sup> plasmid derivatives (a high copy number ColE1-based phagemid, Stratagene Cloning Systems Inc.,

La Jolla CA), PCR cloning plasmids designed for cloning  
Taq-amplified PCR products (e.g., TOPO™ TA Cloning®  
Kit, PCR2.1® plasmid derivatives, Invitrogen, Carlsbad,  
CA), and mammalian, yeast, or virus vectors such as a  
5 baculovirus expression system (pBacPAK plasmid  
derivatives, Clontech, Palo Alto, CA).

After the vector has been constructed and a  
nucleic acid molecule encoding a  $\beta$ 10 polypeptide has  
10 been inserted into the proper site of the vector, the  
completed vector may be inserted into a suitable host  
cell for amplification and/or polypeptide expression.  
The transformation of an expression vector for a  $\beta$ 10  
polypeptide into a selected host cell may be  
15 accomplished by well known methods including methods  
such as transfection, infection, calcium chloride,  
electroporation, microinjection, lipofection or the  
DEAE-dextran method or other known techniques. The  
method selected will in part be a function of the type  
20 of host cell to be used. These methods and other  
suitable methods are well known to the skilled artisan,  
and are set forth, for example, in Sambrook et al.,  
*supra*.

25 Host cells may be prokaryotic host cells (such as  
*E. coli*) or eukaryotic host cells (such as a yeast  
cell, an insect cell or a vertebrate cell). The host  
cell, when cultured under appropriate conditions,  
synthesizes a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10  
30 heterodimer which can subsequently be collected from  
the culture medium (if the host cell secretes it into  
the medium) or directly from the host cell producing it

(if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity, such as glycosylation or phosphorylation, and ease of folding into a biologically active molecule.

A number of suitable host cells are known in the art and many are available from the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209. Examples include, but are not limited to, mammalian cells, such as Chinese hamster ovary cells (CHO) (ATCC No. CCL61) CHO DHFR-cells (Urlaub *et al.*, *Proc. Natl. Acad. Sci. USA*, 97:4216-4220 (1980)), human embryonic kidney (HEK) 293 or 293T cells (ATCC No. CRL1573), or 3T3 cells (ATCC No. CCL92). The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. Other suitable mammalian cell lines, are the monkey COS-1 (ATCC No. CRL1650) and COS-7 cell lines (ATCC No. CRL1651), and the CV-1 cell line (ATCC No. CCL70). Further exemplary mammalian host cells include primate cell lines and rodent cell lines, including transformed cell lines. Normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, as well as primary explants, are also suitable. Candidate cells may be genotypically deficient in the selection gene, or may contain a dominantly acting selection gene. Other suitable mammalian cell lines include but are not limited to, mouse neuroblastoma N2A cells, HeLa, mouse L-929 cells, 3T3 lines derived from Swiss, Balb-c or

NIH mice, BHK or HaK hamster cell lines, which are available from the ATCC. Each of these cell lines is known by and available to those skilled in the art of protein expression.

5

Similarly useful as host cells suitable for the present invention are bacterial cells. For example, the various strains of *E. coli* (e.g., HB101, (ATCC No. 33694) DH5 $\alpha$ , DH10, and MC1061 (ATCC No. 53338)) are well-known as host cells in the field of biotechnology. Various strains of *B. subtilis*, *Pseudomonas spp.*, other *Bacillus spp.*, *Streptomyces spp.*, and the like may also be employed in this method.

Many strains of yeast cells known to those skilled in the art are also available as host cells for the expression of the polypeptides, homodimers or heterodimers of the present invention. Preferred yeast cells include, for example, *Saccharomyces cerevisiae* and *Pichia pastoris*.

Additionally, where desired, insect cell systems may be utilized in the methods of the present invention. Such systems are described for example in Kitts et al., *Biotechniques*, 14:810-817 (1993); Lucklow, *Curr. Opin. Biotechnol.*, 4:564-572 (1993); and Lucklow et al. (*J. Virol.*, 67:4566-4579 (1993)). Preferred insect cells are Sf-9 and Hi5 (Invitrogen, Carlsbad, CA).

30

One may also use transgenic animals to express glycosylated  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. For example, one may use a transgenic

milk-producing animal (a cow or goat, for example) and obtain the present glycosylated polypeptide, homodimer or heterodimer in the animal milk. One may also use plants to produce  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer however, in general, the glycosylation occurring in plants is different from that produced in mammalian cells, and may result in a glycosylated product which is not suitable for human therapeutic use.

### Polypeptide Production

Host cells comprising a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer expression vector may be cultured using standard media well known to the skilled artisan. The media will usually contain all nutrients necessary for the growth and survival of the cells. Suitable media for culturing *E. coli* cells include, for example, Luria Broth (LB) and/or Terrific Broth (TB). Suitable media for culturing eukaryotic cells include Roswell Park Memorial Institute medium 1640 (RPMI 1640), Minimal Essential Medium (MEM) and/or Dulbecco's Modified Eagle Medium (DMEM), all of which may be supplemented with serum and/or growth factors as indicated by the particular cell line being cultured. A suitable medium for insect cultures is Grace's medium supplemented with yeastolate, lactalbumin hydrolysate and/or fetal calf serum, as necessary.

Typically, an antibiotic or other compound useful for selective growth of transformed cells is added as a supplement to the media. The compound to be used will be dictated by the selectable marker element present on

the plasmid with which the host cell was transformed. For example, where the selectable marker element is kanamycin resistance, the compound added to the culture medium will be kanamycin. Other compounds for  
5 selective growth include ampicillin, tetracycline, and neomycin.

The amount of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer produced by a host cell can be  
10 evaluated using standard methods known in the art. Such methods include, without limitation, Western blot analysis, SDS-polyacrylamide gel electrophoresis, non-denaturing gel electrophoresis, HPLC separation, immunoprecipitation, and/or activity assays such as DNA  
15 binding gel shift assays.

If a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer has been designed to be secreted from the host cells, the majority of polypeptide, homodimer or  
20 heterodimer may be found in the cell culture medium. If however, the polypeptide, homodimer or heterodimer is not secreted from the host cells, it will be present in the cytoplasm and/or the nucleus (for eukaryotic host cells) or in the cytosol (for bacterial host  
25 cells).

For  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer situated in the host cell cytoplasm and/or the nucleus (for eukaryotic host cells) or in the  
30 cytosol (for bacterial host cells), intracellular material (including inclusion bodies for gram-negative bacteria) can be extracted from the host cell using any

standard technique known to the skilled artisan. For example, the host cells can be lysed to release the contents of the periplasm/cytoplasm by French press, homogenization, and/or sonication followed by

5 centrifugation.

If the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer has formed inclusion bodies in the cytosol, the inclusion bodies can often bind to the inner and/or

10 outer cellular membranes and thus will be found primarily in the pellet material after centrifugation. The pellet material can then be treated at pH extremes or with a chaotropic agent such as a detergent, guanidine, guanidine derivatives, urea, or urea

15 derivatives in the presence of a reducing agent such as dithiothreitol at alkaline pH or tris carboxyethyl phosphine at acid pH to release, break apart, and solubilize the inclusion bodies. The  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer in its now soluble

20 form can then be analyzed using gel electrophoresis, immuno-precipitation or the like. If it is desired to isolate the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer isolation may be accomplished using standard methods such as those described herein and in

25 Marston et al., *Meth. Enz.*, 182:264-275 (1990).

In some cases, the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may not be biologically active upon isolation. Various methods for "refolding" or

30 converting the polypeptide, homodimer or heterodimer to its tertiary structure and generating disulfide linkages can be used to restore biological activity.

Such methods include exposing the solubilized polypeptide, homodimer or heterodimer to a pH usually above 7 and in the presence of a particular concentration of a chaotrope. The selection of

5 chaotrope is very similar to the choices used for inclusion body solubilization, but usually the chaotrope is used at a lower concentration and is not necessarily the same as chaotropes used for the solubilization. In most cases the refolding/oxidation

10 solution will also contain a reducing agent or the reducing agent plus its oxidized form in a specific ratio to generate a particular redox potential allowing for disulfide shuffling to occur in the formation of the protein's cysteine bridge(s). Some of the commonly

15 used redox couples include cysteine/cystamine, glutathione (GSH)/dithiobis GSH, cupric chloride, dithiothreitol (DTT)/ dithiane DTT, and 2-mercaptoethanol (bME)/dithio-b(ME). A cosolvent may be used to increase the efficiency of the refolding, and

20 the more common reagents used for this purpose include glycerol, polyethylene glycol of various molecular weights, arginine and the like.

If inclusion bodies are not formed to a

25 significant degree upon expression of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer then the polypeptide, homodimer or heterodimer will be found primarily in the supernatant after centrifugation of the cell homogenate. The polypeptide, homodimer or heterodimer

30 may be further isolated from the supernatant using methods such as those described herein.



The purification of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer from solution can be accomplished using a variety of techniques. If the polypeptide, homodimer or heterodimer has been synthesized such that

5 it contains a tag such as Hexahistidine ( $\beta 10$  polypeptide-hexaHis) or other small peptide such as FLAG (Eastman Kodak Co., New Haven, CT) or myc (Invitrogen, Carlsbad, CA) at either its carboxyl or amino terminus, it may be purified in a one-step

10 process by passing the solution through an affinity column where the column matrix has a high affinity for the tag.

For example, polyhistidine binds with great

15 affinity and specificity to nickel, thus an affinity column of nickel (such as the Qiagen® nickel columns) can be used for purification of  $\beta 10$  polypeptide-polyHis. See for example, Ausubel et al., eds., *Current Protocols in Molecular Biology*, Section

20 10.11.8, John Wiley & Sons, New York (1993).

Additionally, the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be purified through the use of a monoclonal antibody which is capable of specifically

25 recognizing and binding to the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer.

Suitable procedures for purification thus include, without limitation, affinity chromatography,

30 immunoaffinity chromatography, ion exchange chromatography, molecular sieve chromatography, High Performance Liquid Chromatography (HPLC),

electrophoresis (including native gel electrophoresis) followed by gel elution, and preparative isoelectric focusing ("Isoprime" machine/technique, Hoefer Scientific, San Francisco, CA). In some cases, two or more purification techniques may be combined to achieve increased purity.

$\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers may also be prepared by chemical synthesis methods (such as solid phase peptide synthesis) using techniques known in the art, such as those set forth by Merrifield et al., *J. Am. Chem. Soc.*, 85:2149 (1963), Houghten et al., *Proc Natl Acad. Sci. USA*, 82:5132 (1985), and Stewart and Young, *Solid Phase Peptide Synthesis*, Pierce Chemical Co., Rockford, IL (1984). Such polypeptides, homodimers or heterodimers may be synthesized with or without a methionine on the amino terminus. Chemically synthesized  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers may be oxidized using methods set forth in these references to form disulfide bridges. Chemically synthesized  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers are expected to have comparable biological activity to the corresponding  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers produced recombinantly or purified from natural sources, and thus may be used interchangeably with a recombinant or natural  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer.

Another means of obtaining a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer according to this

invention is via purification from biological samples such as source tissues and/or fluids in which the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer is naturally found. Such purification can be conducted using methods for protein purification as described herein. The presence of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer during purification may be monitored using, for example, a corresponding antibody prepared against recombinantly produced  $\beta 10$  polypeptide,  $\beta 10$  homodimer,  $\beta 10$  heterodimer or peptide fragments thereof.

A number of additional methods for producing nucleic acids and polypeptides are known in the art, and can be used to produce polypeptides having specificity for  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers of this invention. See for example, Roberts, et al., *Proc. Natl. Acad. Sci.*, 94:12297-12303 (1997), which describes the production of fusion proteins between an mRNA and its encoded peptide. See also U.S. Patent No. 5,824,469, which describes methods of obtaining oligonucleotides capable of carrying out a specific biological function. The procedure involves generating a heterogeneous pool of oligonucleotides, each having a 5' randomized sequence, a central preselected sequence, and a 3' randomized sequence. The resulting heterogeneous pool is introduced into a population of cells that do not exhibit the desired biological function. Subpopulations of the cells are then screened for those which exhibit a predetermined biological function. From that subpopulation,

oligonucleotides capable of carrying out the desired biological function are isolated.

U.S. Patent Nos. 5,763,192, 5,814,476, 5,723,323,  
5 and 5,817,483 describe processes for producing peptides or polypeptides. This is done by producing stochastic genes or fragments thereof, and then introducing these genes into host cells which produce one or more  
10 proteins encoded by the stochastic genes. The host cells are then screened to identify those clones producing peptides or polypeptides having the desired activity.

#### Chemical Derivatives

15 Chemically modified derivatives of the  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers of this invention may be prepared by one skilled in the art, given the disclosures set forth hereinbelow. Such  
20 polypeptide, homodimer or heterodimer derivatives are modified in a manner that is different, either in the type or location of the molecules naturally attached to the polypeptide, homodimer or heterodimer. Derivatives may include molecules formed by the deletion of one or  
25 more naturally-attached chemical groups. The polypeptide comprising the amino acid sequence of SEQ ID NO: 3, a  $\beta 10$ -like polypeptide variant thereof, a  $\beta 10$  homodimer or a  $\beta 10$  heterodimer may be modified by the covalent attachment of one or more polymers. For  
30 example, the polymer selected is typically water soluble so that the protein to which it is attached does not precipitate in an aqueous environment, such as

a physiological environment. Included within the scope of suitable polymers is a mixture of polymers. Preferably, for therapeutic use of the end-product preparation, the polymer will be pharmaceutically  
5 acceptable.

The polymers each may be of any molecular weight and may be branched or unbranched. The polymers each typically have an average molecular weight of between  
10 about 2kDa to about 100kDa (the term "about" indicating that in preparations of a water soluble polymer, some molecules will weigh more, some less, than the stated molecular weight). The average molecular weight of  
15 each polymer preferably is between about 5kDa and about 40kDa, more preferably between about 12kDa and about 40kDa and most preferably between about 20kDa and about 35kDa.

Suitable water soluble polymers or mixtures  
20 thereof include, but are not limited to, N-linked or O-linked carbohydrates, sugars, phosphates, polyethylene glycol (PEG) (including the forms of PEG that have been used to derivatize proteins, including mono-(C<sub>1</sub>-C<sub>10</sub>) alkoxy- or aryloxy-polyethylene glycol), monomethoxy-  
25 polyethylene glycol, dextran (such as low molecular weight dextran, of, for example about 6 kD), cellulose, or other carbohydrate based polymers, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-  
30 polymer, polyoxyethylated polyols (e.g., glycerol) and polyvinyl alcohol. Also encompassed by the present invention are bifunctional crosslinking molecules which may be used to prepare covalently attached multimers of

the polypeptide comprising the amino acid sequence of SEQ ID NO: 3, a polypeptide variant thereof, a  $\beta$ 10 homodimer or a  $\beta$ 10 heterodimer.

5           In general, chemical derivatization may be performed under any suitable condition used to react a protein with an activated polymer molecule. Methods for preparing chemical derivatives of polypeptides, homodimers or heterodimers will generally comprise the  
10 steps of (a) reacting the polypeptide, homodimer or heterodimer with the activated polymer molecule (such as a reactive ester or aldehyde derivative of the polymer molecule) under conditions whereby the polypeptide comprising the amino acid sequence of SEQ  
15 ID NO: 3, or a polypeptide variant thereof, a  $\beta$ 10 homodimer or a  $\beta$ 10 heterodimer becomes attached to one or more polymer molecules, and (b) obtaining the reaction product(s). The optimal reaction conditions will be determined based on known parameters and the  
20 desired result. For example, the larger the ratio of polymer molecules:protein, the greater the percentage of attached polymer molecule. In one embodiment, the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer derivative may have a single polymer molecule moiety at  
25 the amino terminus. See, for example, U.S. Patent No. 5,234,784.

          The pegylation of the polypeptide, homodimer or heterodimer specifically may be carried out by any of  
30 the pegylation reactions known in the art, as described for example in the following references: Francis et al., *Focus on Growth Factors*, 3:4-10 (1992); EP

0154316; EP 0401384 and U.S. Patent No. 4,179,337. For example, pegylation may be carried out via an acylation reaction or an alkylation reaction with a reactive polyethylene glycol molecule (or an analogous reactive water-soluble polymer) as described herein. For the acylation reactions, the polymer(s) selected should have a single reactive ester group. For reductive alkylation, the polymer(s) selected should have a single reactive aldehyde group. A reactive aldehyde is, for example, polyethylene glycol propionaldehyde, which is water stable, or mono C<sub>1</sub>-C<sub>10</sub> alkoxy or aryloxy derivatives thereof (see U.S. Patent No. 5,252,714).

In another embodiment, a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer may be chemically coupled to biotin, and the biotin- $\beta$ 10 polypeptide, biotin- $\beta$ 10 homodimer or biotin- $\beta$ 10 heterodimer molecules which are conjugated are then allowed to bind to avidin, resulting in tetravalent avidin/biotin/ $\beta$ 10 polypeptide molecules, avidin/biotin/ $\beta$ 10 homodimer molecules or avidin/biotin/ $\beta$ 10 heterodimer molecules.  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers may also be covalently coupled to dinitrophenol (DNP) or trinitrophenol (TNP) and the resulting conjugates precipitated with anti-DNP or anti-TNP-IgM to form decameric conjugates with a valency of 10.

Generally, conditions which may be alleviated or modulated by the administration of the present  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer derivatives include those described herein for  $\beta$ 10

polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers.

However, the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer derivatives disclosed herein may have additional activities, enhanced or reduced biological activity, or other characteristics, such as increased or decreased half-life, as compared to the non-derivatized molecules.

#### Genetically Engineered Non-Human Animals

Additionally included within the scope of the present invention are non-human animals such as mice, rats, or other rodents, rabbits, goats, or sheep, or other farm animals, in which the gene (or genes) encoding the native  $\beta$ 10 polypeptide has (have) been disrupted ("knocked out") such that the level of expression of this gene or genes is (are) significantly decreased or completely abolished. Such animals may be prepared using techniques and methods such as those described in U.S. Patent No. 5,557,032.

The present invention further includes non-human animals such as mice, rats, or other rodents, rabbits, goats, sheep, or other farm animals, in which either the native form of the  $\beta$ 10 gene(s) for that animal or a heterologous  $\beta$ 10 gene(s) is (are) over-expressed by the animal, thereby creating a "transgenic" animal. Such transgenic animals may be prepared using well known methods such as those described in U.S. Patent No. 5,489,743 and PCT application No. WO94/28122.



The present invention further includes non-human animals in which the promoter for one or more of the  $\beta 10$  polypeptides is/are either activated or inactivated (e.g., by using homologous recombination methods) to  
5 alter the level of expression of native  $\beta 10$  polypeptide.

These non-human animals may be used for drug candidate screening. In such screening, the impact of  
10 a drug candidate on the animal may be measured. For example, drug candidates may decrease or increase the expression of the  $\beta 10$  gene. In certain embodiments, the amount of  $\beta 10$  polypeptide that is produced may be measured after the exposure of the animal to the drug  
15 candidate. Additionally, in certain embodiments, one may detect the actual impact of the drug candidate on the animal. For example, the overexpression of a particular gene may result in, or be associated with, a disease or pathological condition. In such cases, one  
20 may test a drug candidate's ability to decrease expression of the gene or its ability to prevent or inhibit a pathological condition. In other examples, the production of a particular metabolic product such as a fragment of a polypeptide, may result in, or be  
25 associated with, a disease or pathological condition. In such cases, one may test a drug candidate's ability to decrease the production of such a metabolic product or its ability to prevent or inhibit a pathological condition.

30

#### Microarray

It will be appreciated that DNA microarray

technology can be utilized in accordance with the present invention. DNA microarrays are miniature, high density arrays of nucleic acids positioned on a solid support, such as glass. Each cell or element within the array has numerous copies of a single species of DNA which acts as a target for hybridization for its cognate mRNA. In expression profiling using DNA microarray technology, mRNA is first extracted from a cell or tissue sample and then converted enzymatically to fluorescently labeled cDNA. This material is hybridized to the microarray and unbound cDNA is removed by washing. The expression of discrete genes represented on the array is then visualized by quantitating the amount of labeled cDNA which is specifically bound to each target DNA. In this way, the expression of thousands of genes can be quantitated in a high throughput, parallel manner from a single sample of biological material.

This high throughput expression profiling has a broad range of applications with respect to the  $\beta$ 10 molecules of the invention, including, but not limited to: the identification and validation of  $\beta$ 10 disease-related genes as targets for therapeutics; molecular toxicology of  $\beta$ 10 molecules and inhibitors thereof; stratification of populations and generation of surrogate markers for clinical trials; and enhancing  $\beta$ 10 related small molecule drug discovery by aiding in the identification of selective compounds in high throughput screens (HTS).

Selective Binding Agents

As used herein, the term "selective binding agent" refers to a molecule which has specificity for one or more  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers. Suitable selective binding agents include, but are not limited to, antibodies and derivatives thereof, polypeptides, and small molecules. Suitable selective binding agents may be prepared using methods known in the art. An exemplary  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer selective binding agent of the present invention is capable of binding a certain portion of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer thereby inhibiting the binding of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer to the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor(s).

Selective binding agents such as antibodies and antibody fragments that bind  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers are within the scope of the present invention. The antibodies may be polyclonal including monospecific polyclonal, monoclonal (MAbs), recombinant, chimeric, humanized such as CDR-grafted, human, single chain, and/or bispecific, as well as fragments, variants or derivatives thereof. Antibody fragments include those portions of the antibody which bind to an epitope on the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer. Examples of such fragments include Fab and F(ab') fragments generated by enzymatic cleavage of full-

length antibodies. Other binding fragments include those generated by recombinant DNA techniques, such as the expression of recombinant plasmids containing nucleic acid sequences encoding antibody variable regions.

Polyclonal antibodies directed toward  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer generally are produced in animals (e.g., rabbits or mice) by means of multiple subcutaneous or intraperitoneal injections of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer and an adjuvant. It may be useful to conjugate a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer to a carrier protein that is immunogenic in the species to be immunized, such as keyhole limpet heocyanin, serum, albumin, bovine thyroglobulin, or soybean trypsin inhibitor. Also, aggregating agents such as alum are used to enhance the immune response. After immunization, the animals are bled and the serum is assayed for anti- $\beta 10$  polypeptide, anti- $\beta 10$  homodimer or anti- $\beta 10$  heterodimer antibody titer.

Monoclonal antibodies directed toward  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer are produced using any method which provides for the production of antibody molecules by continuous cell lines in culture. Examples of suitable methods for preparing monoclonal antibodies include the hybridoma methods of Kohler et al., *Nature*, 256:495-497 (1975) and the human B-cell hybridoma method, Kozbor, J. *Immunol.*, 133:3001 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, pp.

51-63 (Marcel Dekker, Inc., New York, 1987). Also provided by the invention are hybridoma cell lines which produce monoclonal antibodies reactive with  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer of this invention.

Monoclonal antibodies of the invention may be modified for use as therapeutics. One embodiment is a "chimeric" antibody in which a portion of the heavy and/or light chain is identical with or homologous to a corresponding sequence in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. Also included are fragments of such antibodies, so long as they exhibit the desired biological activity. See, U.S. Patent No. 4,816,567; Morrison et al., *Proc. Natl. Acad. Sci.*, 81:6851-6855 (1985).

In another embodiment, a monoclonal antibody of the invention is a "humanized" antibody. Methods for humanizing non-human antibodies are well known in the art. See U.S. Patent Nos. 5,585,089, and 5,693,762. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. Humanization can be performed, for example, using methods described in the art (Jones et al., *Nature* 321:522-525 (1986); Riechmann et al., *Nature*, 323:323-327 (1988); Verhoeyen et al., *Science* 239:1534-1536 (1988)), by substituting at least a portion of a

rodent complementarity-determining region (CDR) for the corresponding regions of a human antibody.

Also encompassed by the invention are human  
5 antibodies which bind  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  
 $\beta$ 10 heterodimer. Using transgenic animals (e.g., mice)  
that are capable of producing a repertoire of human  
antibodies in the absence of endogenous immunoglobulin  
production such antibodies are produced by immunization  
10 with a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10  
heterodimer antigen (i.e., having at least 6 contiguous  
amino acids), optionally conjugated to a carrier. See,  
for example, Jakobovits *et al.*, *Proc. Natl. Acad. Sci.*,  
90:2551-2555 (1993); Jakobovits *et al.*, *Nature* 362:255-  
15 258 (1993); Bruggermann *et al.*, *Year in Immuno.*, 7:33  
(1993). In one method, such transgenic animals are  
produced by incapacitating the endogenous loci encoding  
the heavy and light immunoglobulin chains therein, and  
inserting loci encoding human heavy and light chain  
20 proteins into the genome thereof. Partially modified  
animals, that is those having less than the full  
complement of modifications, are then cross-bred to  
obtain an animal having all of the desired immune  
system modifications. When administered an immunogen,  
25 these transgenic animals produce antibodies with human  
(rather than e.g., murine) amino acid sequences,  
including variable regions which are immunospecific for  
these antigens. See PCT application nos.  
PCT/US96/05928 and PCT/US93/06926. Additional methods  
30 are described in U.S. Patent No. 5,545,807, PCT  
application nos. PCT/US91/245, PCT/GB89/01207, and in  
EP 546073B1 and EP 546073A1. Human antibodies may also  
be produced by the expression of recombinant DNA in

host cells or by expression in hybridoma cells as described herein.

In an alternative embodiment, human antibodies can be produced from phage-display libraries (Hoogenboom *et al.*, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991). These processes mimic immune selection through the display of antibody repertoires on the surface of filamentous bacteriophage, and subsequent selection of phage by their binding to an antigen of choice. One such technique is described in PCT Application no. PCT/US98/17364, which describes the isolation of high affinity and functional agonistic antibodies for MPL- and msk-receptors using such an approach.

Chimeric, CDR grafted, and humanized antibodies are typically produced by recombinant methods. Nucleic acids encoding the antibodies are introduced into host cells and expressed using materials and procedures described herein. In a preferred embodiment, the antibodies are produced in mammalian host cells, such as CHO cells. Monoclonal (*e.g.*, human) antibodies may be produced by the expression of recombinant DNA in host cells or by expression in hybridoma cells as described herein.

The anti- $\beta$ 10 polypeptide antibodies, anti- $\beta$ 10 homodimer antibodies or anti- $\beta$ 10 heterodimer antibodies of the invention may be employed in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays (Sola, *Monoclonal Antibodies: A Manual of*

Techniques, pp. 147-158, CRC Press, Inc., 1987) for the detection and quantitation of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. The antibodies will bind the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer with an affinity which is appropriate for the assay method being employed.

For diagnostic applications, in certain embodiments, anti- $\beta$ 10 polypeptide antibodies, anti- $\beta$ 10 homodimer antibodies or anti- $\beta$ 10 heterodimer antibodies may be labeled with a detectable moiety. The detectable moiety can be any one which is capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin; or an enzyme, such as alkaline phosphatase,  $\alpha$ -galactosidase, or horseradish peroxidase (Bayer et al., *Meth. Enz.*, 184:138-163 (1990)).

Competitive binding assays rely on the ability of a labeled standard (e.g., a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer or an immunologically reactive portion thereof) to compete with the test sample analyte (a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer) for binding with a limited amount of anti- $\beta$ 10 polypeptide antibody, anti- $\beta$ 10 homodimer antibody or anti- $\beta$ 10 heterodimer antibody. The amount of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer in the test sample is inversely proportional to the amount of



standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies typically are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies may conveniently be separated from the standard and analyte which remain unbound.

Sandwich assays typically involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected and/or quantitated. In a sandwich assay, the test sample analyte is typically bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three part complex. See, e.g., U.S. Patent No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assays). For example, one type of sandwich assay is an enzyme-linked immunosorbent assay (ELISA), in which case the detectable moiety is an enzyme.

The selective binding agents, including anti- $\beta$ 10 polypeptide antibodies, anti- $\beta$ 10 homodimer antibodies or anti- $\beta$ 10 heterodimer antibodies, also are useful for *in vivo* imaging. An antibody labeled with a detectable moiety may be administered to an animal, preferably into the bloodstream, and the presence and location of the labeled antibody in the host is assayed. The antibody may be labeled with any moiety that is

detectable in an animal, whether by nuclear magnetic resonance, radiology, or other detection means known in the art.

5            Selective binding agents of the invention, including antibodies, may be used as therapeutics. These therapeutic agents are generally agonists or antagonists, in that they either enhance or reduce, respectively, at least one of the biological activities  
10 of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer according to this invention. In one embodiment, antagonist antibodies of the invention are antibodies or binding fragments thereof which are capable of specifically binding to a  $\beta$ 10 polypeptide,  $\beta$ 10  
15 homodimer or  $\beta$ 10 heterodimer and which are capable of inhibiting or eliminating the functional activity of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer *in vivo* or *in vitro*. In preferred embodiments, the selective binding agent, e.g., an antagonist antibody,  
20 will inhibit the functional activity of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer by at least about 50%, and preferably by at least about 80%. In another embodiment, the selective binding agent may be an antibody that is capable of interacting with a  
25  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner (a ligand or receptor) thereby inhibiting or eliminating  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer activity *in vitro* or *in vivo*. Selective binding agents, including agonist and  
30 antagonist anti- $\beta$ 10 polypeptide antibodies, anti- $\beta$ 10 homodimer antibodies or anti- $\beta$ 10 heterodimer

antibodies, are identified by screening assays which are well known in the art.

The invention also relates to a kit comprising  $\beta 10$   
5 polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer selective  
binding agents (such as antibodies) and other reagents  
useful for detecting  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  
 $\beta 10$  heterodimer levels in biological samples. Such  
10 reagents may include, a detectable label, blocking  
serum, positive and negative control samples, and  
detection reagents.

The  $\beta 10$  polypeptide of this invention can be used  
in co-transfection experiments with other polypeptides  
15 to assess formation of heterodimers containing  $\beta 10$   
polypeptide as one of their subunits. The formation of  
such a heterodimer would indicate the potential for  
such a heterodimer to exist *in vivo* and would represent  
a possible  $\beta 10$  heterodimeric hormone. This  
20 heterodimerization assay could be done by co-  
transfecting mammalian cells (COS, 293) with a vector  
capable of expressing a FLAG-tagged  $\beta 10$  polypeptide  
( $\beta 10$ -FLAG) and a vector capable of expressing a tagged  
(but not FLAG tagged) "heterodimer-test" polypeptide.  
25 Conditioned media would be harvested 24-48 hours after  
co-transfection and immunoprecipitation would be  
carried out using a commercially available monoclonal  
antibody directed against the FLAG-tag. The resulting  
immunoprecipitate would be subjected to denaturing  
30 polyacrylamide gel electrophoresis, blotted onto a  
nylon membrane and probed (via Western blot) with an  
antibody capable of specifically recognizing the tagged  
"heterodimer-test" polypeptide. A positive signal on

the Western blot would indicate that  $\beta 10$ -FLAG formed a heterodimer with (and thus co-immunoprecipitated) the tagged "heterodimer-test" polypeptide whereas the absence of a signal on the Western blot would indicate

5 that  $\beta 10$ -FLAG did not form a heterodimer with the tagged "heterodimer-test" polypeptide under the conditions of the assay. As described above in the "Summary of the Invention" section, we used such a heterodimerization assay to determine that  $\beta 10$  forms a

10 heterodimer with human  $\alpha 2$  and have thus discovered and defined a novel heterodimeric glycoprotein hormone,  $\alpha 2/\beta 10$ . Recombinant  $\beta 10$  heterodimeric hormone(s) (without tags), such as  $\alpha 2/\beta 10$ , could be produced in mammalian cells, injected into a mammal

15 (for example, mice) and assessed for *in vivo* function and utility in the diagnosis and/or treatment of one or more of the diseases or disorders listed below.

$\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer

20 of this invention can also be used to clone  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor(s), using an "expression cloning" strategy. Radiolabeled (125-Iodine)  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer or "affinity/activity-

25 tagged"  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer (such as an Fc fusion or an alkaline phosphatase fusion) can be used in binding assays to identify a cell type or cell line or tissue that expresses  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$

30 heterodimer receptor(s). RNA isolated from such cells or tissues would be converted to cDNA, cloned into a mammalian expression vector, and transfected into

mammalian cells (for example, COS, 293) to create an expression library. Radiolabeled or tagged  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer would then be used as an affinity ligand to identify and isolate the subset of cells in this library expressing the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor(s) on their surface. DNA would be isolated from these cells and transfected into mammalian cells to create a secondary expression library in which the fraction of cells expressing  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor(s) would be many-fold higher than in the original library. This enrichment process would be repeated iteratively until a single recombinant clone containing a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor is isolated. Isolation of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor(s) would be very useful in terms of being able to identify or develop novel agonists and antagonists of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer signaling pathway(s). Such agonists and antagonists would include soluble  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer receptor(s), anti- $\beta 10$  polypeptide-receptor(s) antibodies, anti- $\beta 10$  homodimer-receptor(s) antibodies or anti- $\beta 10$  heterodimer(s)-receptor(s) antibodies, small molecules or antisense oligonucleotides, and they could be used in the diagnosis and/or treatment of one or more of the diseases/disorders listed below.

Assaying for other modulators of  $\beta$ 10 polypeptide activity

In some situations, it may be desirable to  
5 identify molecules that are modulators, i.e., agonists  
or antagonists, of the activity of a  $\beta$ 10 polypeptide,  
 $\beta$ 10 homodimer or  $\beta$ 10 heterodimer of this invention.  
Natural or synthetic molecules that modulate the  $\beta$ 10  
polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer may be  
10 identified using one or more screening assays, such as  
those described herein. Such molecules may be  
administered either in an ex vivo manner, or in an in  
vivo manner by injection, or by oral delivery,  
implantation device, or the like.  
15

"Test molecule(s)" refers to the molecule(s) that  
is/are under evaluation for the ability to modulate  
(i.e., increase or decrease) the activity of a  $\beta$ 10  
polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer of this  
20 invention. Most commonly, a test molecule will  
interact directly with the polypeptide, homodimer or  
heterodimer. However, it is also contemplated that a  
test molecule may also modulate  $\beta$ 10 polypeptide,  $\beta$ 10  
homodimer or  $\beta$ 10 heterodimer activity indirectly, such  
25 as by affecting  $\beta$ 10 gene expression, or by binding to a  
 $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer  
binding partner (e.g., receptor or ligand). In one  
embodiment, a test molecule will bind to a  $\beta$ 10  
polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer with an  
30 affinity constant of at least about  $10^{-6}$  M, preferably

about  $10^{-8}$  M, more preferably about  $10^{-9}$  M, and even more preferably about  $10^{-10}$  M.

Methods for identifying compounds which interact  
5 with  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$   
heterodimers of this invention are encompassed by the  
present invention. In certain embodiments, a  $\beta 10$   
polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer is  
10 incubated with a test molecule under conditions which  
permit the interaction of the test molecule with the  
polypeptide, and the extent of the interaction can be  
measured. The test molecule(s) can be screened in a  
substantially purified form or in a crude mixture.

15 In certain embodiments, a  $\beta 10$  polypeptide,  $\beta 10$   
homodimer or  $\beta 10$  heterodimer agonist or antagonist may  
be a protein, peptide, carbohydrate, lipid, or small  
molecular weight molecule which interacts with the  $\beta 10$   
polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer to  
20 regulate its activity. Molecules which regulate  $\beta 10$   
polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer  
expression include nucleic acids which are  
complementary to nucleic acids encoding a  $\beta 10$   
polypeptide of this invention, or are complementary to  
25 nucleic acids sequences which direct, control or  
influence the expression of the  $\beta 10$  polypeptide,  $\beta 10$   
homodimer or  $\beta 10$  heterodimer and which act as anti-  
sense regulators of expression.

30 Once a set of test molecules has been identified  
as interacting with a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or

- $\beta$ 10 heterodimer the molecules may be further evaluated for their ability to increase or decrease  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer activity. The measurement of the interaction of test molecules
- 5 with  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers may be carried out in several formats, including cell-based binding assays, membrane binding assays, solution-phase assays and immunoassays. In general, test molecules are incubated with a  $\beta$ 10
- 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer for a specified period of time, and  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer activity is determined by one or more assays for measuring biological activity.
- 15 The interaction of test molecules with  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers according to this invention may also be assayed directly using polyclonal or monoclonal antibodies in an immunoassay. Alternatively, modified forms of  $\beta$ 10
- 20 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers containing epitope tags as described herein may be used in immunoassays.

- In the event that  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers
- 25 or  $\beta$ 10 heterodimers display biological activity through an interaction with a binding partner (e.g., a receptor or a ligand), a variety of *in vitro* assays may be used to measure the binding of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer to the corresponding
- 30 binding partner (such as a selective binding agent,



receptor, or ligand). These assays may be used to screen test molecules for their ability to increase or decrease the rate and/or the extent of binding of a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer to its binding partner. In one assay, a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer is immobilized in the wells of a microtiter plate. Radiolabeled  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer binding partner (for example, iodinated  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer binding partner) and the test molecule(s) can then be added either one at a time (in either order) or simultaneously to the wells. After incubation, the wells can be washed and counted, using a scintillation counter, for radioactivity to determine the extent to which the binding partner bound to the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer. Typically, the molecules will be tested over a range of concentrations, and a series of control wells lacking one or more elements of the test assays can be used for accuracy in the evaluation of the results. An alternative to this method involves reversing the "positions" of the proteins, i.e., immobilizing  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer binding partner to the microtiter plate wells, incubating with the test molecule and radiolabeled  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer and determining the extent of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer binding. See, for example, chapter 18, *Current Protocols in Molecular Biology*, Ausubel et al., eds., John Wiley & Sons, New York, NY (1995).

As an alternative to radiolabeling, a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer or its respective binding partner may be conjugated to biotin and the presence of biotinylated protein can then be detected using streptavidin linked to an enzyme, such as horseradish peroxidase (HRP) or alkaline phosphatase (AP), that can be detected colorimetrically, or by fluorescent tagging of streptavidin. An antibody directed to a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer or to a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner and conjugated to biotin may also be used and can be detected after incubation with enzyme-linked streptavidin linked to AP or HRP.

A  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer or a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner can also be immobilized by attachment to agarose beads, acrylic beads or other types of such inert solid phase substrates. The substrate-protein complex can be placed in a solution containing the complementary protein and the test compound. After incubation, the beads can be precipitated by centrifugation, and the amount of binding between a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer and its respective binding partner can be assessed using the methods described herein. Alternatively, the substrate-protein complex can be immobilized in a column, and the test molecule and complementary protein are passed through the column. The formation of a complex between a  $\beta$ 10 polypeptide,

$\beta$ 10 homodimer or  $\beta$ 10 heterodimer and its respective binding partner can then be assessed using any of the techniques set forth herein, i.e., radiolabeling, antibody binding, or the like.

5

Another *in vitro* assay that is useful for identifying a test molecule which increases or decreases the formation of a complex between a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer and a corresponding  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner is a surface plasmon resonance detector system such as the BIAcore assay system (Pharmacia, Piscataway, NJ). The BIAcore system may be carried out using the manufacturer's protocol.

This assay essentially involves the covalent binding of either a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer,  $\beta$ 10 heterodimer,  $\beta$ 10 polypeptide binding partner,  $\beta$ 10 homodimer binding partner or  $\beta$ 10 heterodimer binding partner to a dextran-coated sensor chip which is located in a detector. The test compound and the other complementary protein can then be injected, either simultaneously or sequentially, into the chamber containing the sensor chip. The amount of complementary protein that binds can be assessed based on the change in molecular mass which is physically associated with the dextran-coated side of the sensor chip; the change in molecular mass can be measured by the detector system.

In some cases, it may be desirable to evaluate two or more test compounds together for their ability to increase or decrease the formation of a complex between

$\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer and a corresponding  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner. In these cases, the assays set forth herein can be readily modified by

5 adding such additional test compound(s) either simultaneous with, or subsequent to, the first test compound. The remainder of the steps in the assay are as set forth herein.

10 *In vitro* assays such as those described herein may be used advantageously to screen large numbers of compounds for effects on complex formation by the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer and a corresponding  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10

15 heterodimer binding partner. The assays may be automated to screen compounds generated in phage display, synthetic peptide, and chemical synthesis libraries.

20 Compounds which increase or decrease the formation of a complex between a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer and a corresponding  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner may also be screened in cell culture using cells and cell

25 lines expressing either  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer and a corresponding  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner. Cells and cell lines may be obtained from any mammal, but preferably will be from human or other primate,

30 canine, or rodent sources. The binding of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer to cells expressing the corresponding  $\beta$ 10 polypeptide,  $\beta$ 10

homodimer or  $\beta$ 10 heterodimer binding partner at the surface is evaluated in the presence or absence of test molecules, and the extent of binding may be determined by, for example, flow cytometry using a biotinylated  
5 antibody to a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer binding partner. Cell culture assays can be used advantageously to further evaluate compounds that score positive in protein binding assays described herein.

10

Cell cultures can also be used to screen the impact of a drug candidate. For example, drug candidates may decrease or increase the expression of the  $\beta$ 10 gene. In certain embodiments, the amount of  
15  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer that is produced may be measured after exposure of the cell culture to the drug candidate. In certain embodiments, one may detect the actual impact of the drug candidate on the cell culture. For example, the overexpression  
20 of a particular gene may have a particular impact on the cell culture. In such cases, one may test a drug candidate's ability to increase or decrease the expression of the gene or its ability to prevent or inhibit a particular impact on the cell culture. In  
25 other examples, the production of a particular metabolic product such as a fragment of a polypeptide, may result in, or be associated with, a disease or pathological condition. In such cases, one may test a drug candidate's ability to decrease the production of  
30 such a metabolic product in a cell culture.

Therapeutic/Diagnostic Applications of  $\beta 10$  Polypeptides  
and Nucleic Acids

Biological function is anticipated for a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer (such as  $\alpha 2/\beta 10$  heterodimer) similar to that of the glycoprotein hormones FAS, TSH, FSH, LH and CG, which, among other things, are known to act as growth factors in promoting the development (proliferation, differentiation) of prolactin producing cells, the thyroid gland and the gonads. These glycoproteins also act as endocrine hormones in their role as regulators of placental, thyroidal and gonadal function. FAS plays a role in stimulating prolactin secretion from decidual cells in the placenta, TSH plays a major role in the regulation of basal metabolism via the thyroid gland, and FSH, LH and CG play critical roles in male and female fertility, as well as in pregnancy. As such, a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may also play roles in the regulation of basal metabolism, the development/function of the gonads, fertility and pregnancy.

As shown in the example further below,  $\beta 10$  polypeptide is expressed in brain, liver, fetal liver, stomach, pituitary, colon, small intestine, thyroid gland, adrenal gland, pancreas, skin, peripheral blood leucocytes, spleen, testis and placenta. The fact that  $\beta 10$  is expressed in many of the organs and tissues that make up the endocrine system suggests an important role for a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer in the regulation and coordination of one or more endocrine system functions. The endocrine system is known to exert major control over metabolism,

physiological responses to stress, and the development and function of reproductive organs.

The expression of  $\beta 10$  in pituitary, pancreas, 5 adrenal gland, thyroid gland, stomach, small intestine, colon and liver indicates a possible role for a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer in the common function of these organs or tissues, namely, metabolism and energy/nutritional homeostasis (i.e., 10 energy balance, basal metabolic rate, digestion, glucose homeostasis, distribution of body fat, general growth).

The expression of  $\beta 10$  in the pituitary and adrenal 15 glands indicates a possible role for a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer in one of the critical functions subserved by these two important organs, namely, the body's ability to cope with a variety of environmental and physiological stresses (for example, 20 infection, fever, inflammation, fasting, high and low blood pressure, anxiety, shock). Consistent with these possible functions for a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer is the expression of  $\beta 10$  in cells and organs known to be important components of the 25 immune system (peripheral blood leucocytes, spleen, small intestine).

In addition, the expression of  $\beta 10$  in pituitary, testis and placenta indicates a possible role for a  $\beta 10$  30 polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer in the shared function of these organs, specifically, fertility and pregnancy.

$\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may also act as a growth factor involved in the regeneration (proliferation and differentiation) of tissues or specialized cell types present in brain,  
5 liver, stomach, pituitary, colon, small intestine, thyroid gland, adrenal gland, pancreas, skin, peripheral blood leucocytes, spleen, testis and placenta.

- 10 Consistent with the three major areas of potential  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer function, i.e., (1) metabolism and energy/nutritional homeostasis, (2) physiological responses to stress (including immune system function) and (3) fertility  
15 and pregnancy, is the fact that  $\alpha 2$ , which forms a heterodimer with  $\beta 10$ , is expressed (see Example 2 below) in many of the same organs/tissues (anterior pituitary, placenta, pancreas, adrenal cortex, intestinal crypts and gall bladder mucosa) that play  
20 important roles in these 3 major areas.

- Based on the above described potential functions,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be useful for the treatment and/or diagnosis of  
25 metabolic or energy/nutritional homeostatic disorders. Examples of such disorders include, but are not limited to, obesity, wasting syndromes (for example, cancer associated cachexia), myopathies, gastrointestinal disorders, diabetes, growth failure,  
30 hypercholesterolemia, atherosclerosis and aging. Other diseases involving metabolic or energy/nutritional homeostatic disorders are encompassed within the therapeutic and diagnostic utilities that are part of the invention.



Based on the above described potential functions,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be useful for the treatment and/or diagnosis of disorders related to physiological responses to stress (including immune system functions). Examples of such disorders include, but are not limited to, hypertension, immune system dysfunction (for example, excessive inflammation, autoimmune disease, susceptibility to infection such as AIDS, poor wound healing, psoriasis, asthma, arthritis and allergies), shock, anxiety, and high or low blood pressure. Other diseases involving physiological responses to stress, including, but not limited to, immune system functions, are also encompassed within the therapeutic and diagnostic utilities that are part of the invention.

Based on the above described potential functions,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be useful for the treatment and/or diagnosis of disorders related to pregnancy and/or the development and function of reproductive organs. Examples of such disorders include, but are not limited to, infertility, fertility (contraception), impotence, endometriosis, menopause, miscarriage, pre-term labor and delivery. Other diseases involving pregnancy and/or the development and function of reproductive organs are also encompassed within the therapeutic and diagnostic utilities that are part of the invention.

Based on the fact that the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer is likely to have hormone/growth-factor activities,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be useful for the

treatment and/or diagnosis of disorders that could be treated by increasing cell proliferation and/or differentiation. Examples of such disorders include, but are not limited to, tissue damage/degeneration (such as caused by cancer treatments, infections, autoimmune diseases), aging and wound healing. Other diseases that could be treated by increasing cell proliferation and/or differentiation are also encompassed within the therapeutic and diagnostic utilities that are part of the invention.

Based on the fact that the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer is likely to have hormone/growth-factor activities,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be useful for the treatment and/or diagnosis of disorders that could be treated by decreasing cell proliferation and/or differentiation. Examples of such disorders include, but are not limited to, cancers, hyperplasias and hypertrophies. Other diseases that could be treated by decreasing cell proliferation and/or differentiation are also encompassed within the therapeutic and diagnostic utilities that are part of the invention.

Other diseases caused or mediated by undesirable levels of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer are encompassed within the therapeutic and diagnostic utilities that are part of the invention. By way of illustration, such undesirable levels include excessively elevated levels and sub-normal levels.

Compositions and Administration

Therapeutic compositions are within the scope of the present invention. Such pharmaceutical compositions may comprise a therapeutically effective amount of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer,  $\beta$ 10 heterodimer or a  $\beta$ 10 nucleic acid molecule in admixture with a pharmaceutically or physiologically acceptable formulation agent selected for suitability with the mode of administration. Pharmaceutical compositions may comprise a therapeutically effective amount of one or more  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer selective binding agents in admixture with a pharmaceutically or physiologically acceptable formulation agent selected for suitability with the mode of administration.

Acceptable formulation materials preferably are nontoxic to recipients at the dosages and concentrations employed.

The pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. Suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine), antimicrobials, antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite), buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates, other organic acids),

bulking agents (such as mannitol or glycine), chelating agents (such as ethylenediamine tetraacetic acid (EDTA)), complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or  
5 hydroxypropyl-beta-cyclodextrin), fillers, monosaccharides, disaccharides, and other carbohydrates (such as glucose, mannose, or dextrans), proteins (such as serum albumin, gelatin or immunoglobulins), coloring, flavoring and diluting agents, emulsifying  
10 agents, hydrophilic polymers (such as polyvinylpyrrolidone), low molecular weight polypeptides, salt-forming counterions (such as sodium), preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl  
15 alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide), solvents (such as glycerin, propylene glycol or polyethylene glycol), sugar alcohols (such as mannitol or sorbitol), suspending agents, surfactants or wetting agents (such  
20 as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate 80, triton, tromethamine, lecithin, cholesterol, tyloxapal), stability enhancing agents (sucrose or sorbitol), tonicity enhancing agents (such as alkali metal halides  
25 (preferably sodium or potassium chloride), mannitol sorbitol), delivery vehicles, diluents, excipients and/or pharmaceutical adjuvants. (*Remington's Pharmaceutical Sciences*, 18<sup>th</sup> Edition, A.R. Gennaro, ed., Mack Publishing Company [1990]).

30

The optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration,

delivery format, and desired dosage. See for example, *Remington's Pharmaceutical Sciences, supra*. Such compositions may influence the physical state, stability, rate of *in vivo* release, and rate of *in vivo* clearance of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecule.

The primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection, physiological saline solution, or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. Other exemplary pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, which may further include sorbitol or a suitable substitute therefor. In one embodiment of the present invention,  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (*Remington's Pharmaceutical Sciences, supra*) in the form of a lyophilized cake or an aqueous solution. Further, the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer product may be formulated as a lyophilizate using appropriate excipients such as sucrose.

30

The pharmaceutical compositions of this invention can be selected for parenteral delivery. Alternatively, the compositions may be selected for

inhalation or for delivery through the digestive tract, such as orally. The preparation of such pharmaceutically acceptable compositions is within the skill of the art.

5

The formulation components are present in concentrations that are acceptable to the site of administration. For example, buffers are used to maintain the composition at physiological pH or at slightly lower pH, typically within a pH range of from about 5 to about 8.

When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecule in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecule is formulated as a sterile, isotonic solution, properly preserved. Yet another preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (polylactic acid, polyglycolic acid), or beads, or liposomes, that provides for the controlled or sustained release of the product which may then be delivered as a depot injection. Hyaluronic acid may also be used, and this may have the effect of promoting sustained duration in the circulation. Other suitable

means for the introduction of the desired molecule include implantable drug delivery devices.

In one embodiment, a pharmaceutical composition  
5 may be formulated for inhalation. For example, a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecule may be formulated as a dry powder for inhalation.  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer,  $\beta$ 10 heterodimer or  $\beta$ 10 nucleic acid molecule inhalation solutions may also be  
10 formulated with a propellant for aerosol delivery. In yet another embodiment, solutions may be nebulized. Pulmonary administration is further described in PCT application no. PCT/US94/001875, which describes pulmonary delivery of chemically modified proteins.

15

It is also contemplated that certain formulations may be administered orally. In one embodiment of the present invention,  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecules which are administered in  
20 this fashion can be formulated with or without those carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. For example, a capsule may be designed to release the active portion of the formulation at the point in the  
25 gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecule. Diluents, flavorings, low  
30 melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

Another pharmaceutical composition may involve an effective quantity of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer molecules in a mixture with non-toxic excipients which are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or other appropriate vehicle, solutions can be prepared in unit dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See for example, PCT/US93/00829 which describes controlled release of porous polymeric microparticles for the delivery of pharmaceutical compositions. Additional examples of sustained-release preparations include semipermeable polymer matrices in the form of shaped articles, e.g. films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (U.S. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et



al., *Biopolymers*, 22:547-556 (1983)), poly (2-hydroxyethyl-methacrylate) (Langer et al., *J. Biomed. Mater. Res.*, 15:167-277 (1981) and Langer, *Chem. Tech.*, 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., *supra*) or poly-D(-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also may include liposomes, which can be prepared by any of several methods known in the art. See e.g., Eppstein et al., *Proc. Natl. Acad. Sci. USA*, 82:3688-3692 (1985); EP 36,676; EP 88,046; EP 143,949.

The pharmaceutical composition to be used for in vivo administration typically must be sterile. This may be accomplished by filtration through sterile filtration membranes. Where the composition is lyophilized, sterilization using these methods may be conducted either prior to, or following, lyophilization and reconstitution. The composition for parenteral administration may be stored in lyophilized form or in solution. In addition, parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) requiring reconstitution prior to administration.

In a specific embodiment, the present invention is directed to kits for producing a single-dose administration unit. The kits may each contain both a first container having a dried protein and a second  
5 container having an aqueous formulation. Also included within the scope of this invention are kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosyringes).

10 An effective amount of a pharmaceutical composition to be employed therapeutically will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will  
15 thus vary depending, in part, upon the molecule delivered, the indication for which the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer molecule is being used, the route of administration, and the size (body weight, body surface or organ size) and  
20 condition (the age and general health) of the patient. Accordingly, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. A typical dosage may range from about 0.1  $\mu\text{g/kg}$  to up to about 100  $\text{mg/kg}$  or more,  
25 depending on the factors mentioned above. In other embodiments, the dosage may range from 0.1  $\mu\text{g/kg}$  up to about 100  $\text{mg/kg}$ ; or 1  $\mu\text{g/kg}$  up to about 100  $\text{mg/kg}$ ; or 5  $\mu\text{g/kg}$  up to about 100  $\text{mg/kg}$ .

30 The frequency of dosing will depend upon the pharmacokinetic parameters of the  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer molecule in

the formulation used. Typically, a clinician will administer the composition until a dosage is reached that achieves the desired effect. The composition may therefore be administered as a single dose, or as two  
5 or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion via implantation device or catheter. Further refinement of the appropriate dosage is routinely made by those of ordinary skill in the art  
10 and is within the ambit of tasks routinely performed by them. Appropriate dosages may be ascertained through use of appropriate dose-response data.

The route of administration of the pharmaceutical  
15 composition is in accord with known methods, e.g. oral, injection by intravenous, intraperitoneal, intracerebral (intra-parenchymal), intracerebroventricular, intramuscular, intra-ocular, intraarterial, intraportal, or intralesional routes, or  
20 by sustained release systems or implantation device. Where desired, the compositions may be administered by bolus injection or continuously by infusion, or by implantation device.

25 Alternatively or additionally, the composition may be administered locally via implantation of a membrane, sponge, or other appropriate material on to which the desired molecule has been absorbed or encapsulated. Where an implantation device is used, the device may be  
30 implanted into any suitable tissue or organ, and delivery of the desired molecule may be via diffusion, timed release bolus, or continuous administration.

In some cases, it may be desirable to use pharmaceutical compositions according to this invention in an *ex vivo* manner. In such instances, cells, tissues, or organs that have been removed from the patient are exposed to pharmaceutical compositions after which the cells, tissues and/or organs are subsequently implanted back into the patient.

In other cases, a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer of this invention can be delivered by implanting certain cells that have been genetically engineered, using methods such as those described herein, to express and secrete the polypeptide, homodimer or heterodimer. Such cells may be animal or human cells, and may be autologous, heterologous, or xenogeneic. Optionally, the cells may be immortalized. In order to decrease the chance of an immunological response, the cells may be encapsulated to avoid infiltration of surrounding tissues. The encapsulation materials are typically biocompatible, semi-permeable polymeric enclosures or membranes that allow the release of the protein product(s) but prevent the destruction of the cells by the patient's immune system or by other detrimental factors from the surrounding tissues.

Additional embodiments of the present invention relate to cells and methods (e.g., homologous recombination and/or other recombinant production methods) for both the *in vitro* production of therapeutic polypeptides and for the production and delivery of therapeutic polypeptides by gene therapy or cell therapy. Homologous and other recombination

- methods may be used to modify a cell that contains a normally transcriptionally silent  $\beta 10$  gene, or an under expressed gene, and thereby produce a cell which expresses therapeutically efficacious amounts of  $\beta 10$
- 5 polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer.

- Homologous recombination is a technique originally developed for targeting genes to induce or correct mutations in transcriptionally active genes
- 10 (Kucherlapati, *Prog. in Nucl. Acid Res. & Mol. Biol.*, 36:301, 1989). The basic technique was developed as a method for introducing specific mutations into specific regions of the mammalian genome (Thomas et al., *Cell*, 44:419-428, 1986; Thomas and Capecchi, *Cell*, 51:503-
- 15 512, 1987; Doetschman et al., *Proc. Natl. Acad. Sci.*, 85:8583-8587, 1988) or to correct specific mutations within defective genes (Doetschman et al., *Nature*, 330:576-578, 1987). Exemplary homologous recombination techniques are described in U.S. Patent No. 5,272,071
- 20 (EP 9193051, EP Publication No. 505500; PCT/US90/07642, International Publication No. WO 91/09955).

- Through homologous recombination, the DNA sequence to be inserted into the genome can be directed to a
- 25 specific region of the gene of interest by attaching it to targeting DNA. The targeting DNA is a nucleotide sequence that is complementary (homologous) to a region of the genomic DNA. Small pieces of targeting DNA that are complementary to a specific region of the genome
- 30 are put in contact with the parental strand during the DNA replication process. It is a general property of DNA that has been inserted into a cell to hybridize, and therefore, recombine with other pieces of

endogenous DNA through shared homologous regions. If this complementary strand is attached to an oligonucleotide that contains a mutation or a different sequence or an additional nucleotide, it too is  
5 incorporated into the newly synthesized strand as a result of the recombination. As a result of the proofreading function, it is possible for the new sequence of DNA to serve as the template. Thus, the transferred DNA is incorporated into the genome.

10

Attached to these pieces of targeting DNA are regions of DNA which may interact with or control the expression of a  $\beta 10$  polypeptide, e.g., flanking sequences. For example, a promoter/enhancer element, a  
15 suppresser, or an exogenous transcription modulatory element is inserted in the genome of the intended host cell in proximity and orientation sufficient to influence the transcription of DNA encoding the desired  $\beta 10$  polypeptide. The control element controls a  
20 portion of the DNA present in the host cell genome. Thus, the expression of the desired  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer may be achieved not by transfection of DNA that encodes the  $\beta 10$  gene itself, but rather by the use of targeting DNA (containing  
25 regions of homology with the endogenous gene of interest) coupled with DNA regulatory segments that provide the endogenous gene sequence with recognizable signals for transcription of the  $\beta 10$  gene.

30

In an exemplary method, the expression of a desired targeted gene in a cell (i.e., a desired endogenous cellular gene) is altered via homologous

recombination into the cellular genome at a preselected site, by the introduction of DNA which includes at least a regulatory sequence, an exon and a splice donor site. These components are introduced into the

5 chromosomal (genomic) DNA in such a manner that this, in effect, results in the production of a new transcription unit (in which the regulatory sequence, the exon and the splice donor site present in the DNA construct are operatively linked to the endogenous

10 gene). As a result of the introduction of these components into the chromosomal DNA, the expression of the desired endogenous gene is altered.

Altered gene expression, as described herein,

15 encompasses activating (or causing to be expressed) a gene which is normally silent (unexpressed) in the cell as obtained, as well as increasing the expression of a gene which is not expressed at physiologically significant levels in the cell as obtained. The

20 embodiments further encompass changing the pattern of regulation or induction such that it is different from the pattern of regulation or induction that occurs in the cell as obtained, and reducing (including eliminating) the expression of a gene which is

25 expressed in the cell as obtained.

One method by which homologous recombination can be used to increase, or cause,  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer production from a cell's

30 endogenous  $\beta 10$  gene involves first using homologous recombination to place a recombination sequence from a site-specific recombination system (e.g., Cre/loxP, FLP/FRT) (Sauer, *Current Opinion In Biotechnology*,

5:521-527, 1994; Sauer, *Methods In Enzymology*, 225:890-900, 1993) upstream (that is, 5' to) of the cell's endogenous genomic  $\beta 10$  polypeptide coding region. A plasmid containing a recombination site homologous to the site that was placed just upstream of the genomic  $\beta 10$  polypeptide coding region is introduced into the modified cell line along with the appropriate recombinase enzyme. This recombinase causes the plasmid to integrate, via the plasmid's recombination site, into the recombination site located just upstream of the genomic  $\beta 10$  polypeptide coding region in the cell line (Baubonis and Sauer, *Nucleic Acids Res.*, 21:2025-2029, 1993; O'Gorman et al., *Science*, 251:1351-1355, 1991). Any flanking sequences known to increase transcription (e.g., enhancer/promoter, intron, translational enhancer), if properly positioned in this plasmid, would integrate in such a manner as to create a new or modified transcriptional unit resulting in *de novo* or increased  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer production from the cell's endogenous  $\beta 10$  gene.

A further method to use the cell line in which the site specific recombination sequence had been placed just upstream of the cell's endogenous genomic  $\beta 10$  polypeptide coding region is to use homologous recombination to introduce a second recombination site elsewhere in the cell line's genome. The appropriate recombinase enzyme is then introduced into the two-recombination-site cell line, causing a recombination event (deletion, inversion, translocation) (Sauer, *Current Opinion In Biotechnology*, *supra*, 1994; Sauer,



Methods In Enzymology, supra, 1993) that would create a new or modified transcriptional unit resulting in *de novo* or increased  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer production from the cell's endogenous  $\beta 10$  gene.

An additional approach for increasing, or causing, the expression of the  $\beta 10$  polypeptide from a cell's endogenous  $\beta 10$  gene involves increasing, or causing, the expression of a gene or genes (e.g., transcription factors) and/or decreasing the expression of a gene or genes (e.g., transcriptional repressors) in a manner which results in *de novo* or increased  $\beta 10$  polypeptide production from the cell's endogenous  $\beta 10$  gene. This method includes the introduction of a non-naturally occurring polypeptide (e.g., a polypeptide comprising a site specific DNA binding domain fused to a transcriptional factor domain) into the cell such that *de novo* or increased  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer production from the cell's endogenous  $\beta 10$  gene results.

The present invention further relates to DNA constructs useful in the method of altering expression of a target gene. In certain embodiments, the exemplary DNA constructs comprise: (a) one or more targeting sequences; (b) a regulatory sequence; (c) an exon; and (d) an unpaired splice-donor site. The targeting sequence in the DNA construct directs the integration of elements (a)-(d) into a target gene in a cell such that the elements (b)-(d) are operatively linked to sequences of the endogenous target gene. In

another embodiment, the DNA constructs comprise: (a) one or more targeting sequences, (b) a regulatory sequence, (c) an exon, (d) a splice-donor site, (e) an intron, and (f) a splice-acceptor site, wherein the  
5 targeting sequence directs the integration of elements (a)-(f) such that the elements of (b)-(f) are operatively linked to the endogenous gene. The targeting sequence is homologous to the preselected site in the cellular chromosomal DNA with which  
10 homologous recombination is to occur. In the construct, the exon is generally 3' of the regulatory sequence and the splice-donor site is 3' of the exon.

If the sequence of a particular gene is known,  
15 such as the nucleic acid sequence of the  $\beta$ 10 gene presented herein, a piece of DNA that is complementary to a selected region of the gene can be synthesized or otherwise obtained, such as by appropriate restriction of the native DNA at specific recognition sites  
20 bounding the region of interest. This piece serves as a targeting sequence(s) upon insertion into the cell and will hybridize to its homologous region within the genome. If this hybridization occurs during DNA replication, this piece of DNA, and any additional  
25 sequence attached thereto, will act as an Okazaki fragment and will be incorporated into the newly synthesized daughter strand of DNA. The present invention, therefore, includes nucleotides encoding a  $\beta$ 10 polypeptide, which nucleotides may be used as  
30 targeting sequences.

$\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer cell therapy, *e.g.*, the implantation of cells producing

$\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers is also contemplated. This embodiment involves implanting cells capable of synthesizing and secreting a biologically active form of the  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. Such  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer-producing cells can be cells that are natural producers of  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers or may be recombinant cells whose ability to produce  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers has been augmented by transformation with a gene encoding the desired  $\beta$ 10 polypeptide or with a gene augmenting the expression of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. Such a modification may be accomplished by means of a vector suitable for delivering the gene as well as promoting its expression and secretion. In order to minimize a potential immunological reaction in patients being administered a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer as may occur with the administration of a polypeptide of a foreign species, it is preferred that the natural cells producing  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer be of human origin and produce human  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer. Likewise, it is preferred that the recombinant cells producing  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer be transformed with an expression vector containing a gene encoding a human  $\beta$ 10 polypeptide.

30           Implanted cells may be encapsulated to avoid the

infiltration of surrounding tissue. Human or non-human animal cells may be implanted in patients in biocompatible, semipermeable polymeric enclosures or membranes that allow the release of  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer but that prevent the destruction of the cells by the patient's immune system or by other detrimental factors from the surrounding tissue. Alternatively, the patient's own cells, transformed to produce  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers *ex vivo*, may be implanted directly into the patient without such encapsulation.

Techniques for the encapsulation of living cells are known in the art, and the preparation of the encapsulated cells and their implantation in patients may be routinely accomplished. For example, Baetge *et al.* (WO95/05452; PCT/US94/09299) describe membrane capsules containing genetically engineered cells for the effective delivery of biologically active molecules. The capsules are biocompatible and are easily retrievable. The capsules encapsulate cells transfected with recombinant DNA molecules comprising DNA sequences coding for biologically active molecules operatively linked to promoters that are not subject to down regulation *in vivo* upon implantation into a mammalian host. The devices provide for the delivery of the molecules from living cells to specific sites within a recipient. In addition, see U.S. Patent Nos. 4,892,538, 5,011,472, and 5,106,627. A system for encapsulating living cells is described in PCT Application no. PCT/US91/00157 of Aebischer *et al.* See also, PCT Application no. PCT/US91/00155 of Aebischer

et al., Winn et al., *Exper. Neurol.*, 113:322-329 (1991), Aebischer et al., *Exper. Neurol.*, 111:269-275 (1991); and Tresco et al., *ASAIQ*, 38:17-23 (1992).

5           In vivo and in vitro gene therapy delivery of  $\beta$ 10 polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers is also envisioned. One example of a gene therapy technique is to use the  $\beta$ 10 gene (either genomic DNA, cDNA, and/or synthetic DNA) encoding a  $\beta$ 10 polypeptide  
10 which may be operably linked to a constitutive or inducible promoter to form a "gene therapy DNA construct". The promoter may be homologous or heterologous to the endogenous gene, provided that it is active in the cell or tissue type into which the  
15 construct will be inserted. Other components of the gene therapy DNA construct may optionally include, DNA molecules designed for site-specific integration (e.g., endogenous sequences useful for homologous recombination), tissue-specific promoter, enhancer(s)  
20 or silencer(s), DNA molecules capable of providing a selective advantage over the parent cell, DNA molecules useful as labels to identify transformed cells, negative selection systems, cell specific binding agents (as, for example, for cell targeting), cell-  
25 specific internalization factors, and transcription factors to enhance expression by a vector as well as factors to enable vector manufacture.

A gene therapy DNA construct can then be  
30 introduced into cells (either ex vivo or in vivo) using viral or non-viral vectors. One means for introducing the gene therapy DNA construct is by means of viral

vectors as described herein. Certain vectors, such as retroviral vectors, will deliver the DNA construct to the chromosomal DNA of the cells, and the gene can integrate into the chromosomal DNA. Other vectors will  
5 function as episomes, and the gene therapy DNA construct will remain in the cytoplasm.

In yet other embodiments, regulatory elements can be included for the controlled expression of the  $\beta 10$   
10 gene in the target cell. Such elements are turned on in response to an appropriate effector. In this way, a therapeutic polypeptide can be expressed when desired. One conventional control means involves the use of small molecule dimerizers or rapalogs (as described in  
15 WO9641865 (PCT/US96/099486); WO9731898 (PCT/US97/03137) and WO9731899 (PCT/US95/03157) used to dimerize chimeric proteins which contain a small molecule-binding domain and a domain capable of initiating biological process, such as a DNA-binding protein or  
20 transcriptional activation protein. The dimerization of the proteins can be used to initiate transcription of the transgene.

An alternative regulation technology uses a method  
25 of storing proteins expressed from the gene of interest inside the cell as an aggregate or cluster. The gene of interest is expressed as a fusion protein that includes a conditional aggregation domain which results in the retention of the aggregated protein in the  
30 endoplasmic reticulum. The stored proteins are stable and inactive inside the cell. The proteins can be released, however, by administering a drug (e.g., small molecule ligand) that removes the conditional

aggregation domain and thereby specifically breaks apart the aggregates or clusters so that the proteins may be secreted from the cell. See, *Science* 287:816-817, and 826-830 (2000).

5

Other suitable control means or gene switches include, but are not limited to, the following systems. Mifepristone (RU486) is used as a progesterone antagonist. The binding of a modified progesterone  
10 receptor ligand-binding domain to the progesterone antagonist activates transcription by forming a dimer of two transcription factors which then pass into the nucleus to bind DNA. The ligand binding domain is modified to eliminate the ability of the receptor to  
15 bind to the natural ligand. The modified steroid hormone receptor system is further described in U.S. 5,364,791; WO9640911, and WO9710337.

Yet another control system uses ecdysone (a fruit  
20 fly steroid hormone) which binds to and activates an ecdysone receptor (cytoplasmic receptor). The receptor then translocates to the nucleus to bind a specific DNA response element (promoter from ecdysone-responsive gene). The ecdysone receptor includes a  
25 transactivation domain/DNA-binding domain/ligand-binding domain to initiate transcription. The ecdysone system is further described in U.S. 5,514,578; WO9738117; WO9637609; and WO9303162.

30 Another control means uses a positive tetracycline-controllable transactivator. This system involves a mutated tet repressor protein DNA-binding domain (mutated tet R-4 amino acid changes which

resulted in a reverse tetracycline-regulated transactivator protein, i.e., it binds to a tet operator in the presence of tetracycline) linked to a polypeptide which activates transcription. Such  
5 systems are described in U.S. Patent Nos. 5,464,758; 5,650,298 and 5,654,168.

Additional expression control systems and nucleic acid constructs are described in U.S. Patent Nos.  
10 5,741,679 and 5,834,186, to Innovir Laboratories Inc.

*In vivo* gene therapy may be accomplished by introducing the gene encoding a  $\beta 10$  polypeptide into cells via local injection of a  $\beta 10$  nucleic acid  
15 molecule or by other appropriate viral or non-viral delivery vectors. Hefti, *Neurobiology*, 25:1418-1435 (1994). For example, a nucleic acid molecule encoding a  $\beta 10$  polypeptide of this invention may be contained in an adeno-associated virus (AAV) vector for delivery to  
20 the targeted cells (e.g., Johnson, International Publication No. WO95/34670; International Application No. PCT/US95/07178). The recombinant AAV genome typically contains AAV inverted terminal repeats flanking a DNA sequence encoding a  $\beta 10$  polypeptide  
25 operably linked to functional promoter and polyadenylation sequences.

Alternative suitable viral vectors include, but are not limited to, retrovirus, adenovirus, herpes  
30 simplex virus, lentivirus, hepatitis virus, parvovirus, papovavirus, poxvirus, alphavirus, coronavirus, rhabdovirus, paramyxovirus, and papilloma virus



vectors. U.S. Patent No. 5,672,344 describes an *in vivo* viral-mediated gene transfer system involving a recombinant neurotrophic HSV-1 vector. U.S. Patent No. 5,399,346 provides examples of a process for providing  
5 a patient with a therapeutic protein by the delivery of human cells which have been treated *in vitro* to insert a DNA segment encoding a therapeutic protein.

Additional methods and materials for the practice of gene therapy techniques are described in U.S. Patent  
10 No. 5,631,236 involving adenoviral vectors; U.S. Patent No. 5,672,510 involving retroviral vectors; and U.S. 5,635,399 involving retroviral vectors expressing cytokines.

15 Nonviral delivery methods include, but are not limited to, liposome-mediated transfer, naked DNA delivery (direct injection), receptor-mediated transfer (ligand-DNA complex), electroporation, calcium phosphate precipitation, and microparticle bombardment  
20 (e.g., gene gun). Gene therapy materials and methods may also include the use of inducible promoters, tissue-specific enhancer-promoters, DNA sequences designed for site-specific integration, DNA sequences capable of providing a selective advantage over the  
25 parent cell, labels to identify transformed cells, negative selection systems and expression control systems (safety measures), cell-specific binding agents (for cell targeting), cell-specific internalization factors, and transcription factors to enhance  
30 expression by a vector as well as methods of vector manufacture. Such additional methods and materials for the practice of gene therapy techniques are described in U.S. Patent No. 4,970,154 involving electroporation

techniques; WO96/40958 involving nuclear ligands; U.S. Patent No. 5,679,559 describing a lipoprotein-containing system for gene delivery; U.S. Patent No. 5,676,954 involving liposome carriers; U.S. Patent No. 5,593,875 concerning methods for calcium phosphate transfection; and U.S. Patent No. 4,945,050 wherein biologically active particles are propelled at cells at a speed whereby the particles penetrate the surface of the cells and become incorporated into the interior of the cells.

It is also contemplated that  $\beta 10$  gene therapy or cell therapy can further include the delivery of one or more additional polypeptide(s) in the same or a different cell(s). Such cells may be separately introduced into the patient, or the cells may be contained in a single implantable device, such as the encapsulating membrane described above, or the cells may be separately modified by means of viral vectors.

A means to increase endogenous  $\beta 10$  polypeptide expression in a cell via gene therapy is to insert one or more enhancer elements into the  $\beta 10$  polypeptide promoter, where the enhancer element(s) can serve to increase transcriptional activity of the  $\beta 10$  gene. The enhancer element(s) used will be selected based on the tissue in which one desires to activate the gene(s); enhancer elements known to confer promoter activation in that tissue will be selected. For example, if a gene encoding a  $\beta 10$  polypeptide is to be "turned on" in T-cells, the *lck* promoter enhancer element may be used. Here, the functional portion of the transcriptional

element to be added may be inserted into a fragment of DNA containing the  $\beta 10$  polypeptide promoter (and optionally, inserted into a vector and/or 5' and/or 3' flanking sequence(s), etc.) using standard cloning techniques. This construct, known as a "homologous recombination construct", can then be introduced into the desired cells either *ex vivo* or *in vivo*.

Gene therapy can also be used to decrease  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer expression by modifying the nucleotide sequence of the endogenous promoter(s). Such modification is typically accomplished via homologous recombination methods. For example, a DNA molecule containing all or a portion of the promoter of the  $\beta 10$  gene(s) selected for inactivation can be engineered to remove and/or replace pieces of the promoter that regulate transcription. For example the TATA box and/or the binding site of a transcriptional activator of the promoter may be deleted using standard molecular biology techniques; such deletion can inhibit promoter activity thereby repressing the transcription of the corresponding  $\beta 10$  gene. The deletion of the TATA box or the transcription activator binding site in the promoter may be accomplished by generating a DNA construct comprising all or the relevant portion of the  $\beta 10$  polypeptide promoter(s) (from the same or a related species as the  $\beta 10$  gene(s) to be regulated) in which one or more of the TATA box and/or transcriptional activator binding site nucleotides are mutated via substitution, deletion and/or insertion of one or more nucleotides. As a result, the TATA box and/or

activator binding site has decreased activity or is rendered completely inactive. The construct will typically contain at least about 500 bases of DNA that correspond to the native (endogenous) 5' and 3' DNA sequences adjacent to the promoter segment that has been modified. The construct may be introduced into the appropriate cells (either *ex vivo* or *in vivo*) either directly or via a viral vector as described herein. Typically, the integration of the construct into the genomic DNA of the cells will be via homologous recombination, where the 5' and 3' DNA sequences in the promoter construct can serve to help integrate the modified promoter region via hybridization to the endogenous chromosomal DNA.

15

Other Uses of the Nucleic Acids and Polypeptides of this Invention

Nucleic acid molecules of the present invention (including those that do not themselves encode biologically active polypeptides) may be used to map the locations of the  $\beta 10$  gene and related genes on chromosomes. Mapping may be done by techniques known in the art, such as PCR amplification and *in situ* hybridization.

25

$\beta 10$  nucleic acid molecules (including those that do not themselves encode biologically active polypeptides), may be useful as hybridization probes in diagnostic assays to test, either qualitatively or quantitatively, for the presence of a  $\beta 10$  DNA or corresponding RNA in mammalian tissue or bodily fluid samples.

30

The  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers may be used (simultaneously or sequentially) in combination with one or more  
5 cytokines, growth factors, antibiotics, anti-inflammatory, and/or chemotherapeutic agents as is appropriate for the indication being treated.

Other methods may also be employed where it is  
10 desirable to inhibit the activity of one or more  $\beta 10$  polypeptides,  $\beta 10$  homodimers or  $\beta 10$  heterodimers of this invention. Such inhibition may be effected by nucleic acid molecules which are complementary to and hybridize to expression control sequences (triple helix  
15 formation) or to  $\beta 10$  mRNA. For example, antisense DNA or RNA molecules, which have a sequence that is complementary to at least a portion of the selected  $\beta 10$  gene(s) can be introduced into the cell. Anti-sense probes may be designed by available techniques using  
20 the sequence of the  $\beta 10$  polypeptide disclosed herein. Typically, each such antisense molecule will be complementary to the start site (5' end) of each selected  $\beta 10$  gene. When the antisense molecule then hybridizes to the corresponding  $\beta 10$  mRNA, translation  
25 of this mRNA is prevented or reduced. Anti-sense inhibitors provide information relating to the decrease or absence of a  $\beta 10$  polypeptide,  $\beta 10$  homodimer or  $\beta 10$  heterodimer in a cell or organism.

30 Alternatively, gene therapy may be employed to create a dominant-negative inhibitor of one or more  $\beta 10$

polypeptides,  $\beta$ 10 homodimers or  $\beta$ 10 heterodimers. In this situation, the DNA encoding a mutant polypeptide of each selected  $\beta$ 10 polypeptide can be prepared and introduced into the cells of a patient using either

5 viral or non-viral methods as described herein. Each such mutant is typically designed to compete with endogenous polypeptide, homodimer or heterodimer in its biological role.

10 In addition, a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer of this invention, whether biologically active or not, may be used as an immunogen, that is, the polypeptide contains at least one epitope to which antibodies may be raised. Selective binding agents

15 that bind to a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer (as described herein) may be used for *in vivo* and *in vitro* diagnostic purposes, including, but not limited to, use in labeled form to detect the presence of  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10

20 heterodimer in a body fluid or cell sample. The antibodies may also be used to prevent, treat, or diagnose a number of diseases and disorders, including those recited herein. The antibodies may bind to a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer so as to

25 diminish or block at least one activity characteristic of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer, or may bind to a polypeptide to increase at least one activity characteristic of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer (including by increasing

30 the pharmacokinetics of a  $\beta$ 10 polypeptide,  $\beta$ 10 homodimer or  $\beta$ 10 heterodimer).

cDNA encoding  $\beta$ 10 polypeptide in *E. coli* was deposited with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, Virginia  
5 20110-2209, on December 28, 1999, under accession number PTA-1210.

The following examples are intended for illustration purposes only, and should not be construed  
10 as limiting the scope of the invention in any way.

Example 1: DNA Encoding Human Beta-10

The amino acid sequence of CG-(chorionic  
15 gonadotropin)- $\beta$ -subunit was Blasted against an, in house generated, Virtual Protein database derived from public human genomic sequences present in GenBank. A virtual protein containing a 45 amino acid region with significant homology to the carboxy half of CG- $\beta$  was  
20 identified. The short (135 base pair) region of human genomic sequence that encoded the 45 amino acid stretch came from an over 160 kilobase pair GenBank human genomic DNA sequence (accession # AL049871). By  
analyzing an 8 kilobase pair stretch of genomic  
25 sequence just 5' of the 135 base pair sequence, a region having significant homology (and containing a frameshift) to the N-terminal half of CG- $\beta$  was identified. The nucleotide sequence of this novel gene was compiled from the genomic sequences. The amino  
30 acid sequence of this compiled gene had significant homology to the four known human glycoprotein hormone  $\beta$ -subunit polypeptides and had an N-terminal predicted signal peptide, consistent with this novel human gene being a new  $\beta$ -like member of the glycoprotein hormone

family. There was a 4.5-kb intron located between the two putative N-terminal half and C-terminal half coding exons. Intron spanning PCR (see Tissue Expression, Beta-10 section below) of cDNAs from various tissues  
5 sources revealed that  $\beta 10$  was expressed in numerous tissues including pituitary.

The full coding region (ATG to TGA stop codon) and some of the 3'UTR (untranslated region) of  $\beta 10$  was  
10 cloned as one fragment by PCR using the following reaction mix and PCR conditions:

Template: ten microliters of Human Pituitary Marathon Ready cDNA (Clontech Laboratories, Inc., Palo Alto, CA; catalog no. 7424-1). Forward primer: 5'-ATGAAGCTGGCATTCCTCTTCCTT- 3' (SEQ ID NO: 4). Reverse primer: 5'-GCATGTGCTGCTCACACAGGT- 3' (SEQ ID NO: 5). Final concentration of each primer: 1.0 micromolar. Final concentration of dNTPs: 200  
20 micromolar. Five units of Pfu polymerase (Stratagene, La Jolla, CA). Ten microliters of 10x Pfu reaction buffer (Stratagene, La Jolla, CA). Ten microliters of GC melt (Clontech Laboratories, Inc., Palo Alto, CA; Advantage GC cDNA PCR kit; catalog no. K1907-1). Final  
25 reaction volume: 100 microliters. Cycling conditions: 94°C for sixty seconds followed by 45 cycles of 94°C (ten seconds), 60°C (twenty seconds), 72°C (ninety seconds), and then at the end of the 45th cycle an incubation at 72°C for seven minutes, then an  
30 additional 10 cycles of 94°C (ten seconds), 60°C (twenty seconds), 72°C (ninety seconds), and then at the end of the additional 10th cycle an incubation at 72°C for seven minutes.

35 The PCR reaction was run on an agarose gel, and a



single band was seen. This DNA band was cloned into pPCR-Script AMP (Stratagene). The sequence of the insert in one of the resulting clones is that of SEQ ID NO: 2 which contains the full coding region (ATG to TGA stop codon) and some of the 3'UTR (untranslated region) of  $\beta 10$ .

The following is a list and description of  $\beta 10$  sequences from publicly available databases:

10

GenBank Accession # AL049871: 170 kilobase pairs of human genomic sequence. No exons, genes or homologies are identified in this record and the full coding region sequence of  $\beta 10$  is broken up by an intronic sequence.

15

GenBank Accession # AL118555: 126 kilobase pairs of human genomic sequence. No exons, genes or homologies are identified in this record and the full coding region sequence of  $\beta 10$  is broken up by an intronic sequence.

20

#### Example 2: Tissue Expression, Beta-10

Using a PCR fragment as a probe, it was not possible to obtain a hybridization signal on various Human Multiple Tissue Northern Blots (Clontech Inc., Palo Alto, CA). Intron spanning PCR was used to determine the expression pattern of beta-10 as described below.

30

For the Human Sure-RACE Panels (OriGene Technologies, Inc., Rockville, MD; catalog no. HRAA-101) the cDNA samples represented brain, heart, kidney,

- spleen, liver, colon, lung, small intestine, muscle, stomach, testis, placenta, pituitary, thyroid gland, adrenal gland, pancreas, ovary, uterus, prostate, peripheral blood leucocytes, fetal brain, fetal liver, fat and mammary gland. Each cDNA sample was in a separate tube in the form of a dried down pellet of DNA. The reaction mixture was composed as follows:

- Forward primer: 5'-CTGCAGGTGCCTTCGGATC- 3' (SEQ ID NO: 6);  
Reverse primer: 5'-GCATGTGCTGCTCACACAGGT- 3' (SEQ ID NO: 5);  
Amount of each primer: 0.5 picomoles;  
Final concentration of dNTPs: 200 micromolar;  
2.5 microliters of GC melt (Clontech Laboratories, Inc., Palo Alto, CA; Advantage GC cDNA PCR kit; catalog no. K1907-1);  
2.5 units of Taq (Boehringer Mannheim, Indianapolis, IN; PCR Core Kit; catalog no. 1578 553);  
2.5 microliters of 10x PCR-reaction buffer (Boehringer Mannheim, Indianapolis, IN; PCR Core Kit; catalog no. 1578 553);

- For each cDNA sample the above reaction mixture was made up to a volume of 25 microliters, and 20 microliters of this mixture was added to the dried down cDNA pellet. The PCR conditions were as follows: 94°C for sixty seconds, followed by 5 cycles of 94°C (ten seconds) and 72°C (forty seconds), followed by 5 cycles of 94°C (ten seconds) and 70°C (forty seconds), followed by 35 cycles of 94°C (ten seconds) and 68°C (forty seconds), and then followed by 68°C for seven minutes.

- PCR products were then analyzed by agarose gel electrophoresis. The correct size PCR product of 293

base pairs, indicating expression of  $\beta 10$ , was found in colon, small intestine, testis, pituitary and fetal liver.

5           For the Human Rapid-Scan Plate (OriGene Technologies, Inc., Rockville MD; catalog no. HSCA-101) the cDNA samples represented brain, heart, kidney, spleen, liver, colon, lung, small intestine, muscle, stomach, testis, placenta, salivary gland, thyroid  
10   gland, adrenal gland, pancreas, ovary, uterus, prostate, skin, peripheral blood leucocytes, bone marrow, fetal brain and fetal liver. Each cDNA sample was in a separate tube in the form of a dried down pellet of DNA.

15           The reaction mixture that was utilized was as follows:

Forward primer: 5'-CTGCAGGTGCCTTCGGATC- 3' (SEQ ID NO:  
20   6);  
Reverse primer: 5'-GCATGTGCTGCTCACACAGGT- 3' (SEQ ID NO: 5);  
Amount of each primer: 0.5 picomoles;  
Final concentration of dNTPs: 200 micromolar;  
25   2.5 microliters of GC melt (Clontech Laboratories, Inc., Palo Alto, CA; Advantage GC cDNA PCR kit; catalog no. K1907-1);  
2.5 units of Taq (Boehringer Mannheim, Indianapolis, IN; PCR Core Kit; catalog no. 1578 553);  
30   2.5 microliters of 10x PCR-reaction buffer (Boehringer Mannheim, Indianapolis, IN; PCR Core Kit; catalog no. 1578 553);

For each cDNA sample the above reaction mixture  
35   was made up to a volume of 25 microliters, and then 20

microliters of this mixture was added to the dried down cDNA pellet. The PCR conditions were as follows:

- 94°C for sixty seconds followed by 5 cycles of 94°C (ten seconds), 72°C (forty seconds) and then followed  
5 by 5 cycles of 94°C (ten seconds), 70°C (forty seconds) and then followed by 35 cycles of 94°C (ten seconds), 68°C (forty seconds) and then followed by 68°C for seven minutes.

- 10 PCR products were then analyzed by agarose gel electrophoresis. The correct size PCR product of 293 base pairs, indicating expression of  $\beta 10$ , was found in brain, spleen, liver, colon, stomach, placenta, thyroid gland, adrenal gland, pancreas, skin and peripheral  
15 blood leucocytes.

- Combining the expression results from the Human Sure-RACE Panels and the Human Rapid-Scan Plate indicated that  $\beta 10$  is expressed in brain, liver, fetal  
20 liver, stomach, pituitary, colon, small intestine, thyroid gland, adrenal gland, pancreas, skin, peripheral blood leucocytes, spleen, testis and placenta.

25 Example 3: Tissue Expression, Alpha 2

- Northern analysis was carried out to determine the expression pattern of alpha-2. The probe for the Northern was a 390-base pair PCR product  
30 (corresponding to nucleotides 56-445 of SEQ ID NO: 1 from W099/41377). This PCR product was generated via a 466-base pair PCR intermediate as follows:

- PCR was first used to clone a 466-base pair  
35 fragment of alpha-2 from human testis cDNA using the

following reaction mixture and PCR conditions:

- Template: ten microliters of Human Testis Marathon Ready cDNA (Clontech Laboratories, Inc., Palo Alto, CA; catalog no. 7414-1);
- 5 Forward primer: 5'-GAGACATCTCCCCACTGTGTTT-3' (SEQ ID NO: 7);
- Reverse primer: 5'-GTTTCCCCCAACAGAATGTCAA-3' (SEQ ID NO: 8);
- 10 Final concentration of each primer: 1.0 micromolar;  
Final concentration of dNTPs: 200 micromolar;  
Five units of Pfu polymerase;  
Final reaction volume: 100 microliters;  
Cycling conditions: 94°C for sixty seconds followed by
- 15 35 cycles of 94°C (ten seconds), 60°C (thirty seconds), 72°C (sixty seconds), and then at the end of the 35th cycle an incubation at 72°C for five minutes.

- The PCR reaction was run on an agarose gel, and
- 20 four distinct bands were seen. The multiple bands arose from PCR amplification of contaminating human genomic DNA present in the Human Testis Marathon Ready cDNA. The 466-base pair PCR product was isolated from the agarose gel and cloned. A plasmid clone containing
- 25 the 466-base pair sequence was used as a template for generating the 390-base pair PCR fragment using the following reaction mix and PCR conditions:

- Template: ten picograms of the plasmid clone containing
- 30 the above mentioned 466-base pair sequence;
- Forward primer: 5'-ATGCCTATGGCGTCCCCTCAAAC-3' (SEQ ID NO: 9);
- Reverse primer: 5'-CTAGTAGCGAGAGGGCGACACATGTCA-3' (SEQ ID NO: 10);
- 35 Final concentration of each primer: 1.0 micromolar.  
Final concentration of dNTPs: 200 micromolar;

Ten units of Taq polymerase;  
Final reaction volume: 100 microliters;  
Cycling conditions: 94°C for sixty seconds, followed  
by 35 cycles of 94°C (ten seconds), 68°C (sixty  
5 seconds), and then at the end of the 35th cycle an  
incubation at 68°C for six minutes.

The 390-base pair PCR product was then purified by  
agarose gel electrophoresis. This PCR fragment was  
10 labeled with <sup>32</sup>P and hybridized to various Clontech  
Human Multiple Tissue Northern Blots (tissues/cells  
represented were: pancreas, adrenal medulla, thyroid,  
adrenal cortex, testis, thymus, small intestine,  
stomach, spleen, prostate, ovary, colon, peripheral  
15 blood leucocytes, brain, heart, skeletal muscle,  
kidney, liver, placenta and lung) and to a Northern  
blot made with pituitary mRNA using high stringency  
conditions as follows:

20 Hybridization was for one hour at 68°C using  
Clontech "ExpressHyb Hybridization Solution". The  
blots were washed in 2x SSC, 0.1% SDS at room  
temperature twice, for twenty minutes each time. The  
blots were then washed in 0.1x SSC, 0.1% SDS at 50°C  
25 for ten minutes, and then exposed to film.

A strong signal representing a single band was  
obtained in the pancreas mRNA lane and the pituitary  
mRNA lane. A significantly weaker signal was seen in  
30 the placenta mRNA lane.

*In situ* hybridization was done to further  
determine sites of  $\alpha 2$  gene expression. A panel of  
normal embryonic (E10.5 through E18.5) and adult mouse  
35 tissues and adult rhesus monkey tissues were fixed in

4% paraformaldehyde, embedded in paraffin, and sectioned at 5 micrometers. Prior to *in situ* hybridization, tissues were permeabilized with 0.2M HCL, followed by digestion with Proteinase K and acetylation with triethanolamine and acetic anhydride. Sections were hybridized overnight at 55°C with a <sup>33</sup>P-labeled antisense RNA probe complementary to either the mouse or human (for rhesus tissues)  $\alpha 2$  sequence and with sense (control) probes. The antisense and sense <sup>33</sup>P-labeled RNA probes were obtained by *in vitro* transcription of plasmid DNAs containing either the mouse  $\alpha 2$  cDNA (bacterial clone no. 1224990 from the public WashU-HHMI Mouse EST Project) or the human  $\alpha 2$  cDNA (plasmid clone containing the above described PCR generated 390-base pair human  $\alpha 2$  coding region sequence).

Following hybridization, sections were washed in buffer, treated with RNaseA to remove unhybridized probe, and then subjected to a high stringency wash in 0.1X SSC at 55°C. Slides were dipped in Kodak NTB2 emulsion, exposed at 4°C for two-three weeks, developed, and then counterstained. Sections were examined with darkfield and standard illumination to allow simultaneous evaluation of tissue morphology and hybridization signal. The following tissues were then examined:

Mouse tissues: Brain (1 sagittal, 2 coronal sections); GI tract(esophagus, stomach, duodenum, jejunum, ileum, proximal & distal colon); pituitary; liver; lung; heart; spleen; thymus; lymph nodes; kidney; adrenal; bladder; pancreas; salivary gland; male and female reproductive organs (ovary, oviduct and

uterus in the female; testis, epididymus, prostate, seminal vesicle and vas deferens in the male); BAT & WAT (subcutaneous, peri-renal); bone (femur); skin; breast; and skeletal muscle.

5

Rhesus tissues: adrenal gland; liver; gall bladder; intestine; pancreas; and salivary gland.

Both mouse and human antisense probes produced  
10 positive signal detectable above a very low level of background seen with the sense strand controls. In the embryonic mouse, no signal was observed in any major organs from E8.5 through E18.5. At E15.5 and E18.5,  
15 signal was present over scattered cells adjacent to some of the developing bones of the head and teeth. In the adult mouse, a moderate level of signal was present in the adrenal cortex. A lower level of signal was detectable in the anterior and intermediate lobes of the pituitary as well as in intestinal epithelium at  
20 the level of the crypts. In addition, grain density was slightly above background in developing sperm within the seminiferous tubules of the testis and in granulosa cells surrounding developing follicles in the ovary.

25

In rhesus tissues, moderate signal was noted in the adrenal cortex, gall bladder epithelium, and in the intestinal epithelium primarily at the level of the crypts.

30

Combining the expression results from the  $\alpha 2$  Northern and the  $\alpha 2$  *in situ* analysis indicates that  $\alpha 2$  is expressed in anterior pituitary, placenta, pancreas, adrenal cortex, intestinal crypts and gall bladder  
35 mucosa.



WHAT IS CLAIMED

1. An isolated nucleic acid molecule comprising  
5 a nucleotide sequence selected from the group  
consisting of:

(a) the nucleotide sequence set forth in SEQ ID  
NO: 2;

(b) a nucleotide sequence encoding the  
10 polypeptide set forth in SEQ ID NO: 1;

(c) a nucleotide sequence which hybridizes under  
moderately or highly stringent conditions to the  
complement of (a) or (b), wherein the encoded  
polypeptide has an activity of the polypeptide set  
15 forth in SEQ ID NO: 3 or homodimer or heterodimer  
thereof; and

(d) a nucleotide sequence complementary to any of  
(a)-(c).

20 2. An isolated nucleic acid molecule comprising  
a nucleotide sequence selected from the group  
consisting of:

(a) a nucleotide sequence encoding a polypeptide  
that is at least about 70, 75, 80, 85, 90, 95, 96, 97,  
25 98, or 99 percent identical to the polypeptide set  
forth in SEQ ID NO: 1, wherein the polypeptide has an  
activity of the polypeptide set forth in SEQ ID NO: 3  
or homodimer or heterodimer thereof;

(b) a nucleotide sequence encoding an allelic  
30 variant or splice variant of the nucleotide sequence  
set forth in SEQ ID NO: 2, wherein the encoded  
polypeptide has an activity of the polypeptide set  
forth in SEQ ID NO: 3 or homodimer or heterodimer

thereof;

- (c) a nucleotide sequence of SEQ ID NO: 2, (a), or (b) encoding a polypeptide fragment of at least about 25 amino acid residues, wherein the polypeptide
- 5 has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(d) a nucleotide sequence of SEQ ID NO: 2 or (a)-(c) comprising a fragment of at least about 16 nucleotides;

- 10 (e) a nucleotide sequence which hybridizes under moderately or highly stringent conditions to the complement of any of (a)-(d), wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof; and
- 15 (f) a nucleotide sequence complementary to any of (a)-(c).

3. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group
- 20 consisting of:

(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 1 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide set

25 forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 1 with at least one amino acid insertion, wherein the polypeptide has an activity

30 of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(c) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 1 with at least one amino

acid deletion, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(d) a nucleotide sequence encoding a polypeptide  
5 as set forth in SEQ ID NO: 1 which has a C- and/or N-terminal truncation, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(e) a nucleotide sequence encoding a polypeptide  
10 as set forth in SEQ ID NO: 1 with at least one modification selected from the group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of  
15 the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(f) a nucleotide sequence of (a)-(e) comprising a fragment of at least about 16 nucleotides;

(g) a nucleotide sequence which hybridizes under  
20 moderately or highly stringent conditions to the complement of any of (a)-(f), wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof; and

(h) a nucleotide sequence complementary to any of  
25 (a)-(e).

4. A vector comprising the nucleic acid molecule of Claims 1, 2, or 3.

30 5. A host cell comprising the vector of Claim 4.

6. The host cell of Claim 5 that is a eukaryotic cell.

7. The host cell of Claim 5 that is a prokaryotic cell.

8. A process of producing a  $\beta$ 10 polypeptide or  
5  $\beta$ 10 homodimer comprising culturing the host cell of Claim 5 under suitable conditions to express the polypeptide or homodimer, and optionally isolating the polypeptide or homodimer from the culture.

10 9. A polypeptide or homodimer produced by the process of Claim 8.

10. The process of Claim 8, wherein the nucleic acid molecule comprises promoter DNA other than the  
15 promoter DNA for the native  $\beta$ 10 polypeptide operatively linked to the DNA encoding the  $\beta$ 10 polypeptide.

11. The isolated nucleic acid molecule according to Claim 2 wherein the percent identity is determined  
20 using a computer program selected from the group consisting of GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, and the Smith-Waterman algorithm.

12. A process for determining whether a compound  
25 modulates  $\beta$ 10 polypeptide or  $\beta$ 10 homodimer activity or production comprising exposing a cell comprising the vector of claim 4 to the compound, and measuring  $\beta$ 10 polypeptide or  $\beta$ 10 homodimer activity or production in said cell.

30 13. An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 3.

14. An isolated polypeptide comprising the amino

acid sequence selected from the group consisting of:

(a) the mature amino acid sequence as set forth in SEQ ID NO: 3, comprising a mature amino terminus at residue 1, optionally further comprising an amino-terminal methionine;

(b) an amino acid sequence for an ortholog of SEQ ID NO: 3, wherein the encoded polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(c) an amino acid sequence that is at least about 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 percent identical to the amino acid sequence of SEQ ID NO: 3, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(d) a fragment of the amino acid sequence set forth in SEQ ID NO: 3 comprising at least about 25 amino acid residues, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(e) an amino acid sequence for an allelic variant or splice variant of either the amino acid sequence set forth in SEQ ID NO: 3 or at least one of (a)-(c) wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof.

15. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

(a) the amino acid sequence set forth in SEQ ID NO: 3 with at least one conservative amino acid substitution, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof;

(b) the amino acid sequence set forth in SEQ ID NO: 3 with at least one amino acid insertion, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer

5 thereof;

(c) the amino acid sequence set forth in SEQ ID NO: 3 with at least one amino acid deletion, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer

10 thereof;

(d) the amino acid sequence set forth in SEQ ID NO: 3 which has a C- and/or N-terminal truncation, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof; and

15

(e) the amino acid sequence set forth in SEQ ID NO: 3, with at least one modification selected from the group consisting of amino acid substitutions, amino acid insertions, amino acid deletions, C-terminal truncation, and N-terminal truncation, wherein the polypeptide has an activity of the polypeptide set forth in SEQ ID NO: 3 or homodimer or heterodimer thereof.

20

25 16. An isolated polypeptide encoded by the nucleic acid molecule of Claims 1, 2, or 3.

17. The isolated polypeptide according to Claim 14 wherein the percent identity is determined using a computer program selected from the group consisting of GAP, BLASTP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, and the Smith-Waterman algorithm.

30

18. An antibody produced by immunizing an animal with a peptide comprising the amino acid sequence of

35

SEQ ID NO: 3.

19. An antibody or fragment thereof that specifically binds the polypeptide of Claims 13, 14, or 15.

20. The antibody of Claim 19 that is a monoclonal antibody.

21. A hybridoma that produces a monoclonal antibody that binds to a peptide comprising the amino acid sequence of SEQ ID NO: 3.

22. A method of detecting or quantitating the amount of  $\beta$ 10 polypeptide using an anti- $\beta$ 10 antibody or fragment thereof which specifically binds the polypeptide of claims 13, 14 or 15.

23. A selective binding agent or fragment thereof that specifically binds at least one polypeptide, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of:

- a) the amino acid sequence set forth in SEQ ID NO: 3; and
- b) a fragment of the amino acid sequence set forth in SEQ ID NO: 3; and
- c) a naturally occurring variant of (a) or (b).

24. The selective binding agent of Claim 23 that is an antibody or fragment thereof.

25. The selective binding agent of Claim 23 that is a humanized antibody.

26. The selective binding agent of Claim 23 that is a human antibody or fragment thereof.

5 27. The selective binding agent of Claim 23 that is a polyclonal antibody or fragment thereof.

28. The selective binding agent of Claim 23 that is a monoclonal antibody or fragment thereof.

10 29. The selective binding agent of Claim 23 that is a chimeric antibody or fragment thereof.

30. The selective binding agent of Claim 23 that is a CDR-grafted antibody or fragment thereof.  
15

31. The selective binding agent of Claim 23 that is an anti-idiotypic antibody or fragment thereof.

20 32. The selective binding agent of Claim 23 which is a variable region fragment.

33. The variable region fragment of Claim 32 which is a Fab or a Fab' fragment.

25 34. A selective binding agent or fragment thereof comprising at least one complementarity determining region with specificity for a polypeptide having the amino acid sequence of SEQ ID NO: 3.

30 35. The selective binding agent of Claim 23 which is bound to a detectable label.

36. The selective binding agent of Claim 23 which antagonizes  $\beta$ 10 polypeptide biological activity.  
35



37. A method for treating, preventing, or ameliorating a disease, condition, or disorder comprising administering to a patient an effective amount of a selective binding agent according to Claim 23.

38. A selective binding agent produced by immunizing an animal with a polypeptide comprising the amino acid sequence of SEQ ID NO: 3.

39. A hybridoma that produces a selective binding agent capable of binding a polypeptide according to Claims 1, 2, or 3.

40. A composition comprising the polypeptide of Claims 13, 14, or 15 and a pharmaceutically acceptable formulation agent.

41. The composition of Claim 40 wherein the pharmaceutically acceptable formulation agent is a carrier, adjuvant, solubilizer, stabilizer, or anti-oxidant.

42. The composition of Claim 40 wherein the polypeptide comprises the mature amino acid sequence as set forth in SEQ ID NO: 3.

43. A polypeptide comprising a derivative of the polypeptide of Claims 13, 14, or 15.

44. The polypeptide of Claim 43 which is covalently modified with a water-soluble polymer.

45. The polypeptide of Claim 44 wherein the water-soluble polymer is selected from the group consisting of polyethylene glycol, monomethoxy-

polyethylene glycol, dextran, cellulose, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide copolymers, polyoxyethylated polyols, and polyvinyl alcohol.

46. A composition comprising a nucleic acid molecule of Claims 1, 2, or 3 and a pharmaceutically acceptable formulation agent.

10

47. A composition of Claim 46 wherein said nucleic acid molecule is contained in a viral vector.

48. A viral vector comprising a nucleic acid molecule of Claims 1, 2, or 3.

49. A fusion polypeptide comprising the polypeptide of Claims 13, 14, or 15 fused to a heterologous amino acid sequence.

20

50. The fusion polypeptide of Claim 49 wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

51. A method for treating, preventing or ameliorating a medical condition comprising administering to a patient the polypeptide of Claims 13, 14, or 15 or the polypeptide encoded by the nucleic acid of Claims 1, 2, or 3.

30

52. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of Claims 13, 14, or 15

35

or the polypeptide encoded by the nucleic acid molecule of Claims 1, 2, or 3 in a sample; and

- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the  
5 presence or amount of expression of the polypeptide.

53. A device, comprising:

(a) a membrane suitable for implantation; and

- (b) cells encapsulated within said membrane,  
10 wherein said cells secrete a polypeptide of Claims 13, 14, or 15, and wherein said membrane is permeable to said protein and impermeable to materials detrimental to said cells.

54. A method of identifying a compound which  
15 binds to a polypeptide comprising:

(a) contacting the polypeptide of Claims 13, 14, or 15 with a compound; and

- (b) determining the extent of binding of the  
20 polypeptide to the compound.

55. A method of modulating levels of a polypeptide in an animal comprising administering to the animal the nucleic acid molecule of Claims 1, 2,  
25 or 3.

56. A transgenic non-human mammal comprising the nucleic acid molecule of Claims 1, 2, or 3.

57. A homodimer of  $\beta$ 10 polypeptide.

58. A heterodimer of  $\beta$ 10 polypeptide and another polypeptide.

59. The heterodimer of claim 58 in which the other polypeptide is  $\alpha 2$  polypeptide.

5        60. A naturally occurring variant of the  $\beta 10$  homodimer of claim 57 or the  $\beta 10$  heterodimer of claims 58 or 59.

10       61. A vector comprising nucleic acid molecules encoding  $\beta 10$  polypeptide and another polypeptide.

62. The vector of claim 61 in which the other polypeptide is  $\alpha 2$ .

15       63. A host cell comprising the vector of Claim 61.

20       64. The host cell of Claim 63 that is a prokaryotic cell.

65. The host cell of Claim 63 that is a eukaryotic cell.

25       66. A process of producing a heterodimer of  $\beta 10$  and another polypeptide comprising culturing the host cell of Claim 63 under suitable conditions to express the heterodimer, and optionally isolating the heterodimer from the culture.

30       67. The process of claim 66 in which the other polypeptide is  $\alpha 2$ .

68. A heterodimer produced by the process of Claim 66 or 67.

69. A process for determining whether a compound modulates  $\beta 10$  heterodimer activity or production comprising exposing a cell according to Claim 63 to the  
5 compound, and measuring  $\beta 10$  heterodimer activity or production in said cell.

70. An antibody produced by immunizing an animal with a  $\beta 10$  homodimer or  $\beta 10$  heterodimer.  
10

71. An antibody or fragment thereof that specifically binds the  $\beta 10$  homodimer of claim 57 or naturally occurring variant thereof.

15 72. An antibody or fragment thereof that specifically binds the  $\beta 10$  heterodimer of claim 58 or naturally occurring variant thereof.

73. The antibody of Claims 71 or 72 that is a  
20 monoclonal antibody.

74. A hybridoma that produces the monoclonal antibody of claim 73 which is specific to the  $\beta 10$  homodimer.  
25

75. A hybridoma that produces the monoclonal antibody of claim 73 which is specific to a  $\beta 10$  heterodimer.

30 76. A method of detecting or quantitating the amount of  $\beta 10$  homodimer using the antibody of claim 71.

77. A method of detecting or quantitating the amount of a  $\beta 10$  heterodimer using the antibody of

claim 72.

78. A selective binding agent or fragment thereof that specifically binds at least one of the following:

5

a) the  $\beta$ 10 homodimer of claim 57;

b) a fragment of the  $\beta$ 10 homodimer of claim 57;

and

c) a naturally occurring variant of (a) or (b).

10

79. The selective binding agent of Claim 78 that is an antibody or fragment thereof.

80. The selective binding agent of Claim 78 that is a humanized antibody.

15

81. The selective binding agent of Claim 78 that is a human antibody or fragment thereof.

20

82. The selective binding agent of Claim 78 that is a polyclonal antibody or fragment thereof.

83. The selective binding agent Claim 78 that is a monoclonal antibody or fragment thereof.

25

84. The selective binding agent of Claim 78 that is a chimeric antibody or fragment thereof.

85. The selective binding agent of Claim 78 that is a CDR-grafted antibody or fragment thereof.

30

86. The selective binding agent of Claim 78 that is an anti-idiotypic antibody or fragment thereof.

87. The selective binding agent of Claim 78 which is a variable region fragment.

88. The variable region fragment of Claim 87  
5 which is a Fab or a Fab' fragment.

89. A selective binding agent or fragment thereof comprising at least one complementarity determining region with specificity for a  $\beta 10$  homodimer.  
10

90. The selective binding agent of Claim 78 which is bound to a detectable label.

91. The selective binding agent of Claim 78 which  
15 antagonizes  $\beta 10$  homodimer biological activity.

92. A selective binding agent or fragment thereof that specifically binds at least one of the following:

20 a) the  $\beta 10$  heterodimer of claims 58 or 59;

b) a fragment of the  $\beta 10$  heterodimer of claims 58 or 59; and

c) a naturally occurring variant of (a) or (b).

93. The selective binding agent of Claim 92 that is an antibody or fragment thereof.

94. The selective binding agent of Claim 92 that is a humanized antibody.  
30

95. The selective binding agent of Claim 92 that is a human antibody or fragment thereof.

96. The selective binding agent of Claim 92 that

is a polyclonal antibody or fragment thereof.

97. The selective binding agent of Claim 92 that is a monoclonal antibody or fragment thereof.

5

98. The selective binding agent of Claim 92 that is a chimeric antibody or fragment thereof.

99. The selective binding agent of Claim 92 that is a CDR-grafted antibody or fragment thereof.

10

100. The selective binding agent of Claim 92 that is an anti-idiotypic antibody or fragment thereof.

101. The selective binding agent of Claim 92 which is a variable region fragment.

15

102. The variable region fragment of Claim 101 which is a Fab or a Fab' fragment.

20

103. A selective binding agent or fragment thereof comprising at least one complementarity determining region with specificity for a  $\beta$ 10 heterodimer.

104. The selective binding agent of Claim 92 which is bound to a detectable label.

25

105. The selective binding agent of Claim 92 which antagonizes  $\beta$ 10 heterodimer biological activity.

30

106. A method for treating, preventing, or ameliorating a disease, condition, or disorder comprising administering to a patient an effective amount of a homodimer according to claim 57, a heterodimer according to claim 58, or a selective

35



binding agent that specifically binds said homodimer or heterodimer or fragment or naturally occurring variant thereof.

5           107. A composition comprising the homodimer of claim 57, or the heterodimer of claim 58, or a naturally occurring variant of said homodimer or heterodimer, or a fragment of said homodimer or heterodimer, or a selective binding agent of any of the  
10 foregoing, and a pharmaceutically acceptable formulation agent.

15           108. The composition of Claim 107 wherein the pharmaceutically acceptable formulation agent is a carrier, adjuvant, solubilizer, stabilizer, or anti-oxidant.

20           109. The homodimer of Claim 57 or naturally occurring variant thereof which is covalently modified with a water-soluble polymer.

25           110. The homodimer of Claim 109 wherein the water-soluble polymer is selected from the group consisting of polyethylene glycol, monomethoxy-polyethylene glycol, dextran, cellulose, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols, and polyvinyl alcohol.

30           111. A fusion polypeptide comprising the homodimer of Claim 57 or naturally occurring variant thereof which is fused to a heterologous amino acid sequence.

35           112. The fusion polypeptide of Claim 111 wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

113. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

5 (a) determining the presence or amount of expression of the homodimer of Claim 57 or naturally occurring variant thereof; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the  
10 presence or amount of expression of the homodimer.

114. A device, comprising:

(a) a membrane suitable for implantation; and

(b) cells encapsulated within said membrane,  
15 wherein said cells secrete a homodimer of Claim 57 or naturally occurring variant thereof, and wherein said membrane is permeable to said homodimer and impermeable to materials detrimental to said cells.

20 115. A method of identifying a compound which binds to a homodimer comprising:

(a) contacting the homodimer of Claim 57 or naturally occurring variant thereof with a compound;  
and

25 (b) determining the extent of binding of the homodimer to the compound.

116. A method of modulating levels of a homodimer or heterodimer in an animal comprising administering to  
30 the animal the nucleic acid molecule of Claims 1, 2, or 3.

117. A transgenic non-human mammal comprising the nucleic acid molecule of Claims 1, 2, or 3.

118. The heterodimer of Claim 58 or naturally occurring variant thereof which is covalently modified with a water-soluble polymer.

5

119. The heterodimer of Claim 118 wherein the water-soluble polymer is selected from the group consisting of polyethylene glycol, monomethoxy-polyethylene glycol, dextran, cellulose, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols, and polyvinyl alcohol.

120. A fusion polypeptide comprising the heterodimer of Claim 58 or naturally occurring variant thereof fused to a heterologous amino acid sequence.

121. The fusion polypeptide of Claim 120 wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

122. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the heterodimer of Claim 58 or naturally occurring variant thereof; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the heterodimer.

123. A device, comprising:

(a) a membrane suitable for implantation; and

(b) cells encapsulated within said membrane, wherein said cells secrete a heterodimer of Claim 58 or naturally occurring variant thereof, and wherein said membrane is permeable to said heterodimer and  
5 impermeable to materials detrimental to said cells.

124. A method of identifying a compound which binds to a heterodimer comprising:

(a) contacting the heterodimer of Claim 58 or  
10 naturally occurring variant thereof with a compound;  
and

(b) determining the extent of binding of the heterodimer to the compound.

Abstract

Novel  $\beta 10$  polypeptides, including homodimers and heterodimers thereof, and nucleic acid molecules encoding the same are disclosed. The invention also provides vectors, host cells, selective binding agents, and methods for producing  $\beta 10$  polypeptides (as well as homo- and heterodimeric forms). Also provided for are methods for the treatment, diagnosis, amelioration, or prevention of diseases with  $\beta 10$  polypeptides,  $\beta 10$  homodimers and  $\beta 10$  heterodimers or their respective binding agents.

Fig. 1

Human glycoprotein hormone  $\beta$ 10 polypeptide:

MKLAFLLGPMALLLAGYCVLGASSEHLRTFVGCAREFTFLAKKPCRGRLRTITDACWRCETWEKPILEPFYIEAHRIVCYNNETKQVTVKLPNCAKGVDPFYTPVVAIRCDGACSTATTCEETI

Nucleic acid encoding human glycoprotein hormone  $\beta$ 10 polypeptide:

ATGAAGCTGGCAITCCTCTTCCTTGGCCCCCATGGCCCTCCTCCTTCTGGC  
TGGCTATGGCTGTGTCCTCGGTGCCCTCCAGTGGAACTTGCACCTTTG  
TGGCTGTGCCGTGAGGAGTTTACTTTCTTGGCCAAAGAGCCAGCTGC  
AGGGCCCTTCGGATCACACCGATGCCTCGTGGGTCTGTGAGACCTG  
GGAGAAACCCATTCTGGAAACCCCTATATTGAAGCCCATCATCGAGTCT  
GTACCTAACAGAGACCAACAGGTGACTGTCAAGTGGCCCACTGTGCC  
CCGGAGTCGACCCCTTACACTATCCGTGGCCATCCGCTGTGACTG  
CGGAGCTGTCTCCTGTCACCGAGTGTGAGACCATCTGAGGCCCGCT  
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

[illegible]

TO: HUMAN  $\beta$ 10      CHECK: 6611    FROM: 1    TO: 106

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	129
RATIO:	1.321	GAPS:	4
PERCENT SIMILARITY:	47.368	PERCENT IDENTITY:	36.842

```

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
      | = IDENTITY
      : = 2
      . = 1

```

HUMAN TSH- $\beta$  X HUMAN  $\beta$ 10

```

1 .....FCIPTEYTMHIERRECAYLITNTTICAGYCMTRDINGK 40
  | | | | | | | | | | | | | | | | | | | | | | | |
1 ASSGNLRTFVGCAVREFTFPLAKKPGCR.GLRITTDACWGRCETWE..KPI 47
  | | | | | | | | | | | | | | | | | | | | | | | |
41 FLPKYALSQD.VCTYRDFIYRTVEIPGCLPHVAPYFSYPVALSCKGKCN 89
  | | | | | | | | | | | | | | | | | | | | | | | |
48 LEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYFVAIRCDCGACS 97
  | | | | | | | | | | | | | | | | | | | | | | | |
90 TDYSDCIHEAIKTNCTKPQKSYLVGFSV 118
  | | | | | | | | | | | | | | | | | | | | | | | |
98 TATTEC..ETI..... 106
  | | | | | | | | | | | | | | | | | | | | | | | |

```

## Fig. 2B

GAP OF: HUMAN FSH- $\beta$  CHECK: 8841 FROM: 1 TO: 111  
TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	156	LENGTH:	122
RATIO:	1.472	GAPS:	3
PERCENT SIMILARITY:	44.211	<b>PERCENT IDENTITY:</b>	<b>35.789</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):  
| = IDENTITY  
: = 2  
. = 1

HUMAN FSH- $\beta$  X HUMAN  $\beta$ 10

```
1 .....NSCELTNITIAIEKEEERFCISINTTWCAGYCYTRDL.VYK 40
   | . | . | | : | | | | | : : .
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTFVATQCHCGKCDS 80
   | : | | | | | | | | | . | | | .
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
   . | : | | :
100 TTECETI..... 106
```



## Fig. 2C

GAP OF: HUMAN LH- $\beta$  CHECK: 5679 FROM: 1 TO: 121

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003

QUALITY:	140	LENGTH:	125
RATIO:	1.321	GAPS:	3
PERCENT SIMILARITY:	44.118	<b>PERCENT IDENTITY:</b>	<b>32.353</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):  
| = IDENTITY  
: = 2  
. = 1

HUMAN LH- $\beta$  X HUMAN  $\beta$ 10

```

1  .SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPTMMR.VLQ 46
   ||||| . | ||| : : | | | | | : : |
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEPIL 49

47 AVLPLLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFFVALSCRCGPCRRS 96
   ||||| : : . : || | |||| . : ||| : | || | .
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYFVAIRCDCGACSTA 99

97 TSDCGGPKDHP LTC DHPQLSGLLFL 121
   | . : |
100 TTECETI..... 106

```

[illegible]

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

```

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
      | = IDENTITY
      : = 2
      . = 1

```

```

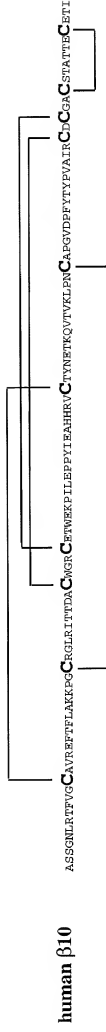
1  _SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPMTMR.VLQ 46
   |||||      |||||      |||||      |||||      |||||
1  ASSGNLRITFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEITWEKPILE 49
   |||||      |||||      |||||      |||||      |||||

47  GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 96
   |||||      |||||      |||||      |||||      |||||
50  PPYIEAHHRVCTYNETKQVTVTKLPNCAPGVDPFYTYPAVIRCDGACSTA 99
   |||||      |||||      |||||      |||||      |||||

97  TTDCGGPKDHLPLTCDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 145
   |||||
100 TTECETI..... 106

```

**Fig. 3**



**DECLARATION AND POWER OF ATTORNEY**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first, and sole inventor (if only one name is listed below) or a joint inventor (if plural names are listed below) of the invention entitled

**BETA-LIKE GLYCOPROTEIN HORMONE POLYPEPTIDE AND HETERODIMER**

which is described and claimed in the specification which:

- ☒ is attached hereto.  
☐ was filed on \_\_\_\_\_  
 as Application Serial No. \_\_\_\_\_  
 and was amended on \_\_\_\_\_ (if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, § 1.56 (a).

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

PRIOR FOREIGN APPLICATION(S)			
Country	Application Number	Filing Date (day, month, year)	Priority Claimed

I hereby claim the benefit under Title 35, United States Code, § 119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S)	
Application Number	Filing Date (day, month, year)
60/192,654	March 28, 2000
60/199,211	April 24, 2000

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of this application is not disclosed in the prior United States application

**DECLARATION AND POWER OF ATTORNEY (cont'd)**

in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the filing date of this application:

PRIOR U.S. APPLICATIONS		
APPLICATION SERIAL NO.	FILING DATE	STATUS

**Power of Attorney:** As a named inventor I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith:

Richard J. Mazza (Reg. No. 27,657), Steven M. Odre (Reg. No. 29,094), Ron K. Levy (Reg. No. 31,539), Scott N. Bernstein (Reg. No. 38,827), Joseph W. Bullock (Reg. No. 37,103), Robert R. Cook (Reg. No. 31,602), Monique L. Cordray (Reg. No. 34,802), Craig A. Crandall (Reg. No. 38,416), Daniel R. Curry (Reg. No. 32,727), Joan D. Eggert (Reg. No. 32,980), Timothy J. Gaul (Reg. No. 33,111), Matthew W. Knight (Reg. No. 36,846), Karen L. Nicastro (Reg. No. 35,968), Nancy A. Oleski (Reg. No. 34,688), Karol M. Pessin (Reg. No. 34,899), Frank S. Ungemach (Reg. No. 34,449), Stuart L. Watt (Reg. No. 32,511), Wendy A. Whiteford (Reg. No. 36,964), Robert B. Winter (Reg. No. 34,458), Thomas D. Zindrick (Reg. No. 32,185), said attorney(s)/agent(s) to have in addition full power of revocation, including the power to revoke any power herein granted.

Please send all future correspondence to:

U.S. Patent Operations/RJM  
Dept. 4300, M/S 27-4-A  
AMGEN INC.  
One Amgen Center Drive  
Thousand Oaks, California 91320-1799

Direct Telephone Calls To:

Richard J. Mazza  
Attorney/Agent for Applicants  
Registration No.: 27,657  
Phone: (805) 447- 4112

**DECLARATION AND POWER OF ATTORNEY (cont'd)**

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Full Name of Sole  
or First Inventor:

Christopher J. R. Paszty

Inventor's Signature:

Christopher Paszty

Date:

11/27/2000

Residence and  
Post Office Address:

1027 Westridge Drive  
Ventura, California 93003, U.S.A.

(Address, City, State, Zip Code, Country)

Citizenship:

USA

Full Name of Second  
Joint Inventor, if Any:

Jin Cao

Inventor's Signature:

Jin Cao

Date:

11/27/2000

Residence and  
Post Office Address:

5731 Etiwanda Avenue, No. 5  
Tarzana, California 91366, U.S.A.

(Address, City, State, Zip Code, Country)

Citizenship:

USA

Full Name of Third  
Joint Inventor, if Any:

Jianhua Gong

Inventor's Signature:

Jianhua Gong

Date:

11/27/2000

Residence and  
Post Office Address:

2489 Girlington Circle  
Thousand Oaks, California 91362, U.S.A.

(Address, City, State, Zip Code, Country)

Citizenship:

China

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant(s): Christopher J. R. Paszty, Jin Cao, and Jianhua Gong  
Serial No.: Not Assigned Yet  
Filed: November 27, 2000  
For: Beta-Like Glycoprotein Hormone Polypeptide and Heterodimer  
Docket No.: A-676A

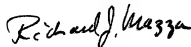
**ATTORNEY'S STATEMENT PURSUANT TO 37 CFR § 1.821**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

I hereby state that the paper copy and the computer readable form (CRF) of the "Sequence Listing" submitted herewith for the above-mentioned patent application are the same.

Respectfully submitted,



Richard J. Mazza  
Attorney/Agent for Applicant(s)  
Registration No.: 27,657  
Phone: (805) 447-4112  
Date: November 27, 2000

Please send all future correspondence to:

U.S. Patent Operations/RJM  
Dept. 4300, M/S 27-4-A  
AMGEN INC.  
One Amgen Center Drive  
Thousand Oaks, California 91320-1799

**EXPRESS MAIL CERTIFICATE**

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Lynne Buchsbaum  
Printed Name

Lynne Buchsbaum  
Signature

## SEQUENCE LISTING

<110> Paszty, Christopher J. R.  
Cao, Jin  
Gong, Jianhua

<120> Beta-Like Glycoprotein Hormone Polypeptide and  
Heterodimer

<130> A-676A

<140> N/A

<141> 2000-11-27

<150> 60/192,654

<151> 2000-03-28

<150> 60/199,211

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